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April 26, 2003, 06:48:54; Search time 40.2691 Seconds (without alignments) 1899.367 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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3054
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Perfect score:
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	Description	Human membrane or	Amino acid sequenc	Amino acid sequenc	Hydrophobic domain	Human isomerase ho	Amino acid sequenc	Amino acid sequenc	Human pancreatic c	Human ovarian anti	Ourself memid forton
SUMMARIES	ΩI	AAB88320	AAY23886	AAG79226	AAB12128	AAY52294	AAY23887	AAY23885	AAB54356	ABP41125	1100000
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	Query Match Length DB	570	541	582	582	582	388	441	434	166	1241
de	Query Match	98.3	94.4	57.1	57.0	57.0	52.6	45.8	44.3	27.2	0 70
	Score	3001	2883	1744	1742	1742	1606	1399	1354	831	760
	Result No.	1	7	٣	4		9	7	æ	6	9

Nucleic acids encoding secretory proteins/membrane proteins, useful in

WPI; 2001-093989/11.

N-PSDB; AAF93747.

Hayashi

Human prostate can Amino acid sequenc Human polypeptide	DIOSOFILIA METANOS NOVEL CENTRAL NEVY HUMAN POLYPEPTIGE NOVEL NUMAN CALCIU	phila mel ted prote secreted PRO1304	ono 4	81 81 81 81 81	Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Polypeptide fragme Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human DITHP polype
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737	291 291 291	5 6 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	268 268 259.5 259.5 259.5	2000 2000 2000 2000 2000 2000 2000	253 253 249.5 247 247 247 247
112	112 112 114	321032	4 6 6 6 6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	, 6, 6, 4, 4, 4, 4, 4, 4, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6,

RESULT 1

ALIGNMENTS

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Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                 Sugiyama T,
                                                          Human membrane or secretory protein clone PSEC0007.
                                                                                                                                                                                                                                 Kawai Y,
        AAB88320 standard; Protein; 570 AA.
                                                                                                                                                                                                                                 Nishikawa T,
                                                                                                                                                                            08-JUL-1999; 99JP-0194179.
11-JAN-2000; 2000JP-0118775.
02-MAY-2000; 2000JP-0183766.
                                                                                                                                                           07-JUL-2000; 2000EP-0114090.
                                           (first entry)
                                                                                                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                 Ota T, Isogai T,
                                                                                                       Homo sapiens.
                                                                                                                         EP1067182-A2.
                                         23-MAY-2001
                                                                                                                                          10-JAN-2001
                          AAB88320;
AAB88320
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This invention relates to nucleic acid sequences AAF93744 - AAF93916
which encode human secretory or membrane proteins represented by
AAB88317 - AAB88419. Included in the Invention are primers
AAF893917 - AAF84295 and AAF62212 - AAF62235 which are used to isolate the
converse, which can be used in vections. The polynucleotides methods for
the production of antibodies directed against the proteins, and cDNA
sequences, which can be used in vaccines. The polynucleotide sequences
can be used in gene therapy. The polynucleotide sequences and the
corrections they encode may be used in the prevention, treatment and
diagnosis of diseases associated with inappropriate secretory
protein/membrane protein expression. The nucleic acids and complementary
correction/membrane protein expression and function of secretory proteins/membrane
corrections may also be used as DNA probes in diagnostic assays
corrections and also be used as DNA probes in diagnostic assays
corrected and their role in metabolism. The polypeptides may be used
consect to study the expression and function of secretory proteins/membrane
polypeptides and their role in metabolism. The polypeptides may be used
as antigens in the production of antibodies against them and in assays to
dentify modulators (agonists and antagonists) of expression and
activity. The antibodies and antagonists may also
corrected agents to down regulate expression and activity. The antibodies may also
corrected agents for detecting the presence of the
colypeptides in samples (e.g. by enzyme linked immunosorbant assay
corrected and diabetes.

Corrected and diabetes. gene therapy or as candidate target molecules in drug development -Claim 1; SEQ ID 8; 609pp + CD ROM; English.

570 AA; Sequence

ö 180 240 240 300 360 420 420 480 480 540 61 YVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNE 120 121 RVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDG 180 61 YVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNE 120 Gaps 1 MAFRGWRPPPPPLLLLLLWVTGQAAPVAGLGSDAELQIERRFVPDECPRTVRSGDFVRYH 60 1 MAFRGWRPPPPPLLLLLLWVTGQAAPVAGLGSDAELQIERRFVPDECPRTVRSGDFVRYH 60 121 GVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDG 181 TLFDSSHNRWKTYDTYVGIGWLIPGMDKGLLGWCVGEKRIITPPFLAYGEDGDGKDIPG GSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGL 481 PEGYMFIWNGEVSPNLFEBIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKN 181 TLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPG QASLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYS 301 RNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGNIPGSAVLVFDIH VIDFHNPSDSISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVL 421 GSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELPELVAGL PEGYMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKN ö 98.3%; Score 3001; DB 22; Length 570; 98.9%; Pred. No. 1.7e-282; ive 0; Mismatches 6; Indels 0; Matches 562; Conservative Similarity Query Match Local 361 481 241 421 g g ò g g 셤 ద ð ò g ò g ò à à Š

541 MFTNQDRNGDGKVTAEEFKLKDQEAKHD 568

AAY23886

AAY23886 standard; Protein; 541 AA.

21-SEP-1999 (first entry)

Human; FK506 binding protein; FKBP65; immune system disorder; immune cell; hematopoletic cell disorder; thrombolytic activity; blood coagulation disorder; blood platelet disorder; wound; heart attack; stroke; scarring; autoimmune disorder; allergic reaction; asthma; allergic asthma; respiratory problem; anaphylaxis; hypersensitivity; blood group incompatibility; organ rejection; graft versus host disease; inflammatory condition; sischmia-reperfusion injury; endoctoin lethality; arthritis; complement-mediated hyperacute rejection; nephritis; lung injury; inflammatory bowel disease; Crohn's disease; infection. Amino acid sequence of a FK506 binding protein.

domo sapiens

WO9935160-A1

15-JUL-1999.

36-JAN-1999;

99WO-US00120.

(HUMA-) HUMAN GENOME SCI INC.

98US-0070875.

39-JAN-1998;

Moore PA, Ruben SM,

WPI; 1999-430382/36. N-PSDB; AAX86147.

New nucleic acids encoding human FK506 binding proteins

Claim 12; Fig 3; 87pp; English.

The present sequence represents human FK506 binding protein 65 (FKBP65).

The polypeptide or polynucleotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain types of hematopoeitic cells. They can be used to modulate in certain types of hematopoeitic cells. They can be used to modulate in certain types of hematopoeitic cells. They can be used to modulate coagulation disorders, blood platelet disorders or wounds resulting from trauma, surgery or other causes, or a decrease can treat heart attacks, trauma, surgery or other causes, or a decrease can treat heart attacks, coher respiratory problems, anaphylaxis, hypersensitivity to an antigenic cother respiratory problems, anaphylaxis, hypersensitivity to an antigenic cother respiratory problems, anaphylaxis, both chronic and acute, including inflammation associated with infection, ischemia-reperfusion injury, endediction or strakes, or commonatibility, organ rejection or graft versus conditions will all the complement-mediated hyperacute rejection, conditions, both chronic and acute, including inflammation associated with infection, ischemia-reperfusion injury, endecrease, or crown, sethabality, arthritis, complement-mediated hyperacute rejection, the particular, fungal and parasitic infections.

541 AA; Sequence

Gaps .; 0 Length 541; Indels 94.4%; Score 2883; DB 20; 100.0%; Pred. No. 4.7e-271; iive 0; Mismatches 0; Conservative Query Match Best Local Similarity Matches 541;

MFTNQDRNGDGKVTAEEFKLXDQEAKHD 568

541

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                                           61 YVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNE 120
                                120
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Kishimoto T;
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                                                                                                                                               RNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGNIPGSAVLVFDIH
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QASLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYS
                                  YVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; neurotrophic factor; PSEC56; nerve growth factor;
neurite outgrowth; neural disease; dementia; cerebral embolism;
spinal injury; peripheral nerve disease.
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Hashimoto K,
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Isogai T, Kawasaki M,
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Nishikawa T,
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Neurotrophic factor expression-inducing agent, applicable in developing drugs for neural diseases e.g. dementia, cerebral embolism, spinal injury and peripheral nerve diseases by screening their regulatory effect
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                                                                                                      The present sequence represents a human neurotrophic factor expression-inducing agent. The polypeptide is designated PSEC56. The PSEC56 protein is used to increase nerve growth factor providing neurite outgrowth effect, which is applicable in developing drugs for neural diseases e.g. dementia, cerebral embolism, spinal injury and peripheral nerve diseases, with use of PSEC56 as the neurotrophic factor expression-inducing agent which can be applied in a system to study induction and secretion mechanism of neurotrophic factor.
                                                                                                                                                                                                                                                                                                                                                          116 AYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PP-----PLLLLLLWVT------GQAAPVAGLGSDAELQIERRFVPDECPRTVRSGD
                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                      Length 582;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                      Query Match 57.1%; Score 1744; DB 22; Best Local Similarity 56.4%; Pred. No. 2.7e-160; Matches 326; Conservative 99; Mismatches 131;
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                                                                                   Example 1; Page 34-38; 42pp; Japanese.
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Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopolesis activity, tissue growth activity, and tunoun and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                               Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosupressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 FVRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKL 115
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Hydrophobic domain protein from clone HP02991 isolated from KB cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 PP-----PLLLLLLWVT-----GQAAPVAGLGSDAELQIERRFVPDECPRTVRSGD 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 230-232; 410pp; English.
                                                                                                                                                                                                                                                                                                              98JP-0326255.
98JP-0364315.
99JP-0069811.
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N-PSDB; AAA62001, AAA62011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease, and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEGENE
                                                                                                                                                                                                     WO200029448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             SAGAMI
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                            17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                     27-APR-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                    22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                    6-MAR-1999;
                                                                                                                                                                                                                                         25-MAY-2000
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Matches 326;
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peptidyl-prolyl cis/trans isomerase; FK506; rapamycin; signalling pathway; T-cell; cancer; leukaemia; testicular cancer; melanoma; immune disorder; asthma; atherosclerosis; diagnosis; treatment; prevention; detection; agonist; antagonist; expression; activity; antibody; apoptosis; gene therapy; genetic immunisation; vaccine.
                                                                                                                  413
                                                                                                                                                                                                        482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "FKBP-type peptidyl-prolyl cis/trans isomerase signature sequence"
236 KDIPGQASLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLF 295
                           303
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                                                                                                                                               423
                                                                                                                                                                           414 KTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEX 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Endoplasmic reticulum targetting sequence"
                                                                         SREDGLPTGYLEVWHKDPPANLFEDMDLNKDGEVPPEEFSTFIKAQVSEGKGRLMPGQD
               244 TVIPPOASLVFHVLLIDVENPKDAVOLETLELPPGCVRRAGAGDFMRYHYNGSLMDGTLF
                                                                                                                                                                                             424 APQEATIGANKVIEGLDTGLQCMCVGERRQLIVPPHLAHGESGARG-VPGSAVLLFEVEL
                                                         DSSYSRNRTFDTYIGOGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAV
                                                                                                                    LVFDIHVIDFHNPSDSISITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLG
                                                                                                                                                                                                                                      474 LELVAGLPEGYMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Phosphorylated by casein kinase II"
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                                                                                                                                                                                                                                                                                                 534 AELIVKNMFTNQDRNGDGKVTAEEFKL---XDQEAKHD 568
                                                                                                                                                                                                                                                                                                               | ::|| ||||| |||:| :| || ||:| 543 PEKTIGDMFQNQDRNQDGKITVDELKLKSDEDEERVHE 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human isomerase homologue; HIH; FKBP65; PPlase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human isomerase homologue-1 (HIH-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    AAY52294 standard; Protein; 582 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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TIJDGTSFDISYSKGGTYDTYVGSGWLIKGMDQGLLGMCPGERRKIIIPPFLAYGEKGYG 243

184

176 TFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDG

8 8 8

582 AA;

Sequence

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418
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Modified-site
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                                                                                    12-DEC-1997;
                                                                                         12-DEC-1997;
                                                                              23-NOV-1999
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This sequence represents human isomerase homologue-1 (HIH-1).

CC Nucleotides encoding HIH-1 were first identified in an ovarian tumour CC Nucleotides encoding HIH-1 were first identified in an ovarian tumour CC CDNA library, the CDNA encoding this sequence being a consensus. HIH-1 is also expressed in other cancerous *cissues, lymph nodes, inflamed CC colon, and synovium. HIH-1 has chemical and structural homology with couse FREPSE, sharing 8% identity as well as the isomerase signature sequence, the endoplasmic retriculum targetting sequence and many of the potential phosphorylation sites. FKEPS (FK506 binding proteins) are a consense of family of peptidyl-proly cisyl-furans isomerases (PPISES) which catalyse CC family of peptidyl-proly cisyl-furans isomerases (PPISES) and crashlyse cc the cis to trans isomerisation of certain proline imidic bonds in CC proteins. FKEPS can bind the potent immunosuppressants FK506 and crapamycin, inhibiting PPISES activity and thus blocking stynalling pathways in T-cells. The expression pattern of HIH-1 and its homology with FKEPSE indicate that it plays a role in cancers (e.g., asthma and catherosclerosis). HIM proteins, and the nucleotides that encode them, may be used for the diagnosis, treatment or prevention of such diseases. HIM condour activity, and to raise antibodies. The antibodies and antagonists of anyoptosis, and the antibodies may also be used in detection of HIM moleotides may be used to downregulate expression and/or activity and increase condours and diagnosis of associated diseases. HIM mucleotides may be used in gene therapy or in the production of recombinant protein represent
                                                                                                                                                    "Phosphorylated by cAMP/cGMP-dependent protein kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                casein kinase II"
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301
/note= "Phosphorylated by casein kinase
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                                                                                                  note= "N-glycosylated"
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563
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391
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                                                                                                                                                                        124 GYGSIGLAGLIPPDATLYFDVVLLDVWNKEDTVQVSTLLRPPHCPRWVQDGDFVRYHYNG 183
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                                                   10 PP-----PILLLLLWVT-----GQAAPVAGLGSDAELQIERRFVPDECPRIVRSGD
                                                                      56 FVRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKQQLITGMDQALVGMCVNERRFVKIPPKC
                           22;
    Length 582;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a FK506 binding protein 65.
57.0%; Score 1.7.2.;
56.4%; Pred. No. 4.3e-160;
+ive 99; Mismatches 131;
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                              Matches 326; Conservative
                   Similarity
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(HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                WPI; 1999-430382/36
                                                                                                                                                                                  N-PSDB; AAX86148
                                 06-JAN-1999;
                                                                09-JAN-1998;
15-JUL-1999
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New nucleic acids encoding human FK506 binding proteins

Claim 12; Fig 4; 87pp; English.

The present sequence represents a human FK506 binding protein 65

(FKB65). It is a splice variant of the sequence given in AAX86147.

The polypeptide or polymenteotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. They may be useful in treating or detecting deficiencies or calls. They may be useful in treating or detecting deficiencies or proliferation of hematopoietic cells, to increase differentiation and proliferation of hematopoietic cells including the pluripocent stem cells, in an effort to treat those disorders associated with a decrease in certain types of hematopoeitic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood coagulation disorders, blood platelet disorders or wounds resulting from trauma, surgery or other causes, or a decrease can treat heart attacks, etcokes or scarring. They can also treat autoimmune disorders, allergic reactions and conditions such as actima (particularly allergic asthma) or other respiratory problems, anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility, organ rejection or graft versus host disease, inflammatory conditions, both chronic and acute, including inflammation associated with infection, ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, orthrine or chemokine induced lung injury, inflammatory bowel disease, or Crohn's disease. They can also be used to treat viral, bacterial, fungal and parasitic infections.

388 AA; Sequence

ö 434 255 NPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 314 61 NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120 315 IPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFHNPSDSISIT 374 EMCVGEKRIVII PPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMFIWNGEVSP 494 241 BMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEVSP 300 195 TYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 254 0; Gaps 1 TYGEIGWLIPGWDKGLLGMCVGBKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 60 375 SHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR 52.6%; Score 1606; DB 20; Length 388; 98.1%; Pred. No. 3.8e-147; tive 1; Mismatches 5; Indels 0; Matches 302; Conservative Query Match Best Local Similarity 495 NLFEEIDK 502 435 셤 g ò 셤 ò සු ò ò g ð

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immune cell; hematopoletic cell disorder; thrombolytic activity; blood coagulation disorder; blood platelet disorder; wound; heart attack; stroke; stroke; scarring; autoimune disorder; allergic reaction; asthma; allergic asthma; respiratory problem; anaphylaxis; hypersensitivity; blood group incompatibility; organ rejection; graft versus host disease; inflammatory condition; ischemia-reperfusion injury; endotoxin lethality; arthritis; complement-mediated hyperacuce rejection; nephritis; lung injury; inflammatory bowel disease; Crohn's disease; infection.
                                                                                               Human; FK506 binding protein; FKBP65; immune system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding human FK506 binding proteins
                                                                          Amino acid sequence of a FK506 binding protein 65.
         AAY23885 standard; Protein; 441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 2; 87pp; English.
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                                                    21-SEP-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-430382/36.
N-PSDB; AAX86146.
                                                                                                                                                                                                                       Homo sapiens.
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AAY2388
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The present sequence represents a human FKS06 binding protein 65

(FKBP65). It is a splice variant of the sequence given in AAX86145.

The polypepited or polynucleotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells, to increase differentiation and proliferation of hematopoietic cells including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain types of hematopoeitic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood coagulation disorders, blood platelet disorders or wounds resulting from trauma, surgery or other causes, or a decrease can treat heart attacks, strokes or scarring. They can also treat autoimmune disorders, altergic reactions and conditions such as asthma (particularly allergic asthma) or other respiratory problems, anabyllasis, hypersensitivity to an antigenic molecule, or blood group incompatibility, organ rejection or cor other respiratory problems, anabyllasis, hypersensitivity to an articlemic molecule, or blood group incompatibility, organ rejection or complement-mediated hyperacular neglection, inflammatory conditions, both chronic and complement-mediated hyperacular rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, or cohn's disease, or complement-mediated byperacular rejection, bacterial, fungal and conditions in the process or search or conditions or complement-mediated byperacular rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, or crohn's disease, they can also be used to treat viral, bacterial, fungal and parasitic infections.

441 AA; Sequence

301 NLFEEINK 308

Gaps 9 Length 441; Indels Query Match 45.8%; Score 1399; DB 20; Best Local Similarity 58.0%; Pred. No. 6.1e-127; Matches 255; Conservative 77; Mismatches 102;

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Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                      372
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                                                                                                                                                                                                                                                                                                                                        360 PPANLFEDIDLNKOGEVPPEEFSTFIKAQVSEGKGRLAMPGQDPEKTIGDMFQNQDRNQDG 419
                                                                           120
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                                                                  DIYVGSGWLIKGMDQGLLGMCPGBRRKIIIPPPLAYGBKGYGTVIPPQASLVFHVLLIDV
                                                                                                                                                                                                                                                                                                                         VSPNLFEEI DKDGNGEVLLEEFSEY IHAQVASGKGKLAPGFDAEL I VKNMFTNQDRNGDG
                                                                                                                                                           VIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSIS
                                                                                                                                                                                                               ITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDM
                                                                                                                                                                                                                                                                    GLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVPDIEXLELVAGLPEGYMFIWNGE
              DTYVGIGWLIPGWDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDL
                                                                                                       HNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGY
134 FDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pancreatic cancer antigen protein sequence SEQ ID NO:808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1260-1261; 1379pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB54356 standard; Protein; 434 AA.
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420 KITVDELKLKSDEDBERVHE 439
                                                                                                                                                                                                                                                                                                                                                                               KVTABEFKL---XDQEAKHD 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000; 2000WO-US05989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC99121.
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AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to proteins, called pancreatic cancer antigens have cytostatic, cardiant and antiantacy, relaxant, contraceptive, courrective, nootropic, immunomodulatory, relaxant, contraceptive, courrective, nootropic, immunomodulatory, relaxant, contraceptive, conversing, cardiant and antianflammatory activities, and can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and exceptibility to one in a conversion or be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.

Conversion and antagonists to the antigens can be screened for. The pancreatic cancer antigen polymucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage cand diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypetides, including contine or be used to treat or prevent neural; immune system, muscular, creproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99212 to AAC99240 and AAB54467 represent cycles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 DMDLNKDGEVPPEEFSTFIKAQVSEGKGRLAMPGQDPEKTIGDMFQNQDRNQDGKITVDEL 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 SIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGGGYVIPGMDE 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 WLIKGWDGGLLGMCPGERRKIIIPPFLAYGEKGYGTVIPPQASLVFHVLLIDVHNPKDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 GLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISITSHYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEKRTVI I PPHLGYGEAGVDGEVPGSAVLVFDI EXLELVAGL PEGYMFI WNGEVSPNL FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.3%; Score 1354; DB 21;
57.5%; Pred. No. 1.4e-122;
ive 76; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AA;
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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; finflammatory condition; limmune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; neurological disorder; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive. (HUMA-) HUMAN GENOME SCI INC. 07-JUN-2001; 2001WO-US18569. 07-JUN-2000; 2000US-209467P. Birse CE, Rosen CA; WPI; 2002-147878/19. N-PSDB; ABQ54202 WO200200677-A1. Homo sapiens. 03-JAN-2002.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases

Claim 11; SEQ ID No 2257; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56315), and also encompasses polypeptides 90% identical and polybuclectides 95% identical to the sequences of the invention. The invention additionally relates to excombinant vectors and host cells comprising human ovarian antigens, and the use of ovarian antigens, and host cells comprising human ovarian antigens, and the use of ovarian antigens, and host cells comprising human ovarian antigens, and the use of ovarian antigen polymuclectides and polypeptides in diagnosing or preventing various ovary and/or breast-related disorders (e.g., infertility, disorders of pregnancy, anovulation, prognosing or preventing various ovary and/or breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system of bloodvers (e.g., infertility, disorders, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic of immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus, tempiratory disorders (e.g., anaemia), cardiors oophoritis, and acquired inferior disorders, neurological disorders gastrointestinal disorders and uniary system disorders. Ovarian antigen polypeptides and conditions of individuals and in forensic analysis, and the collymuclectides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymuclectides may also be used in screening for compounds which independent of individuals and in forensic analysis, and the collypeptides may be used as food additives or to prepare antibodies desquence represents a human ovarian aftigen of the invention. The polymuclectides was cheared and prepare antibodies of the promoter of the sequence data for this parent did not form part of the printed or the sequence data for this parent did not form part of the promoter of the fire of the promoter of the fire of the fire of ftp.wipo.int/pub/published_pct_sequences.

Sequence

; 0 0; Gaps Ouery Match 27.2%; Score 831; DB 23; Length 166; Best Local Similarity 94.4%; Pred. No. 2.1e-72; Matwhes 153; Conservative 4; Mismatches 5; Indels C

107 RFVKIPPKLAYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVS 166

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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO 167 DEVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPF 226 64 DFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPF 123 and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. 4 RLVKIPPKLAYGSEGVSGVIPPDSVLHFDVLLMDIWNSEDQVQVHTYFTPPSCPRTIQVX 63 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder. The invention relates to isolated polynucleotide (I) and 227 LAYGEDGDGKDIPGQASLVFDVALLDLHNPKDSISIENKVVP 268 124 LAYGEEGDGKDIPGQASLVFDVALLDLHNPKDGISIENKVVP 165 Claim 20; SEQ ID No 36270; 103pp; English. Novel human diagnostic protein #5902. ABG05911 standard; Protein; 1241 AA. 30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167. 13-FEB-2002 (first entry) Drmanac RT, Liu C, WPI; 2001-639362/73. (HYSE-) HYSEQ INC. N-PSDB; AAS70098 WO200175067-A2. Homo sapiens. biodiversity 11-OCT-2001. ABG05911; RESULT 10 ð ద ð g

polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymorleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity at ftp.wipo.int/pub/published_pct_sequences 1241 AA; Sequence

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invention.
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                   12;
                                                                                                                     341
                                                                                                                                                                     460 EVPGSAVLVPDIEXLEL-----IWN-- 489
                                                                                                                                                                                                                                                                                              364 NYGEKSQQCAEEEGDIEWQLNASVLVAQAQEASLYEDRIITREKDMRRVRDEPEKVVKQW 423
                                                                             ----IPGQASLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFL 281
                                                                                        126 RYHYNGSLMDGTLFDSSYSRNHTYNTYIGQGYIIPGMDQGLQGACMGBRRRITIPPHLAY 185
                                                                                                                                                          GEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISITSHYKPPD-CSVLSKKGDYLKYHYNAS 399
                                                                                                                                                                                                 LLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDG 459
                   Gaps
                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate cancer associated gene sequences, referred to as prostate
                                                                                                                                                                                                                                                            304 VTKIVSVVLKYLYAYELHPCIQKNWWEEKIPLAKTTLEKTWLFHEIGRCYLELDQAWQAQ
                                                                                                                                                                                                                                                                                --GEVSPNLPEE---IDKDGNGEVLL---EEFSEYIHAQVASGKGKLAPGFDAELIVKNM
                                                                                                                     TYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGY
                                                    6 WIADQGHGPGAAGHVSWREKEIIIPPPLAYGEKGYGEGGKGHKGKFRRRGKNQASTYSCS
                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer antigen protein sequence SEQ ID NO:1692.
                     Indels
24.9%; Score 760; DB 22; 1 39.4%; Pred. No. 4e-64; ive 62; Mismatches 117;
                                       WLI-PGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKD---
                                                                                                                                                                                                                                                                                                                         542 FTNQDRNGDGKVTAEEFKLXDQEA 565
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                                                                                                                                                                                                                                                                                                                                                                                            AAB57114 standard; Protein; 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US05988
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                     Conservative
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  Query Match
Best Local Similarity
Matches 175; Conserv
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                                                                                                                                                                                                                                           The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, amphrotropic, antiinfective, synaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polymucleotides may be used for detection of prostate cancer, chromosome infantification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, dispatchintestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAP16506 to AAP16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                  to AAF16505 encode the human prostate cancer associated called prostate cancer antigens, given in AAB56363 to AAB57302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; FK506 binding protein; FKBP65; immune system disorder; immune cell; hematopoietic cell disorder; thrombolytic activity; blood platelet disorder; wound; blood coagulation disorder; blood platelet disorder; wound; heart attack; stroke scarring; autoimmune disorder; allergic reaction; asthma; allergic asthma; respiratory problem; anaphylaxis; hypersensitivity; blood group incompatibility; organ rejection; graft versus host disease; inflammatory condition; ischemia-reperfusion injury; endotoxin lethality; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CILHEGIQPRIQGG------MKSTL------GATKKGCFGRAWMLTLVIPALWE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 KVVPENCERISOSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGY----VIPGMDE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH------NPKDSISIEN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HKGKFRRGKNOASTYSCSG 304
antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 WRLPRSPSLPAVPTPGTMFPAGPPSHSLLRLPLLQLLLLVVQAVGRGLGRASPAGGPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 FKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDQALVGMCVNERRFVKIPPKLAYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of FK506 binding protein 65 (FKBP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 WRPP----PLLLLLWVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.3%; Score 743; DB 21; 43.5%; Pred. No. 2.6e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45; Mismatches
                                                                                                                  Claim 11; Page 2162-2164; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPGERRKIIIPPFLAYGEKGYGEG--GOG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY23884 standard; Protein; 316 AA
                                                 disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 GLLGVCIGEKRXIVVPPHL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.3°
Best Local Similarity 43.5°
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:: | | | AKAGGSRGQEIETTVKPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 AA;
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AAO05027 standard; Protein; 127 AA.

RESULT 13

Human polypeptide SEQ ID NO 18919.

(first entry)

06-NOV-2001 AAO05027;

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complement-mediated hyperacute rejection; nephritis; lung injury; inflammatory bowel disease; Crohn's disease; infection.
                                                                                                                     New nucleic acids encoding human FK506 binding proteins
                                                                                                                                  Claim 12; Fig 1; 87pp; English.
                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                        Wei Y;
                                                                 98US-0070875.
                                                     99WO-US00120
                                                                                        Moore PA, Ruben SM,
                                                                                                    1999-430382/36.
                                                                                                          N-PSDB; AAX86145
                                                     06-JAN-1999;
                                                                 39-JAN-1998;
                  Homo sapiens
                             WO9935160-A1
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The present sequence represents human FK506 binding protein 65 (FKBP65).

The polypeptide or polymucleotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemocaxis) of immune cells. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells, to increase differentiation and proliferation of hematopoietic cells including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain types of hematopoietic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood conquisation disorders, blood platelet disorders or wounds resulting from trauma, surgery or other causes, or a decrease can treat heart attacks, trocks or scarring. They can also treat autoimmune disorders, allergic reactions and conditions such as asthma (patricularly allergic activity to an antigenic molecule, or blood group incompatibility, organ rejection or graft versus host disease, inflammatory conditions, both chronic and acute, including inflammation associated with infection, isochemia-reportusion injury, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, or Crohn's disease. They can also be used to treat viral, bacterial, fungal and parasitic infections.

56 FVRYHYVGTPPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKL 115 64 FVRYHYNGTFEDGKKFDSSYDRNTLVAIVVGVGRLIIGMDRGLMGMCVNERRRLIUPPHL 123 116 AYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNG 175 176 TFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDG 235 10 PP-----PLLLLLLWVT-----GQAAPVAGLGSDAELQIERRFVPDECPRTVRSGD 55 6 PPSHSILRLPLIQLILLVVQAVGRGLGRASPAGGPLED--VVIERYHIPRACPREVQMGD 63 Query Match
24.1%; Score 737; DB 20; Length 316;
Best Local Similarity 58.1%; Pred: No. 8e-63;
Matches 140; Conservative 35; Wismatches 50; Indels 16 316 AA; 236 K 236 244 E 244 Sequence d g 셤 ò 셤 ઠે ઠે ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                         Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TVIIPPHLGYGEAGYDGEVPGSAVLMFDIELLELVAGLPEGYMFIWNGEVSPNLFEEIDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 SVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKR 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMFIWNGEVSPNLFEEIDK 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 21.3%; Score 651; DB 22; Local Similarity 97.6%; Pred. No. 4.4e-55; new 123; Conservative. 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAI84958
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                                                                                                                                                                                                                            Homo sapiens.
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hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest, cerebrovascular disorder; ischaemia; angiogenesis; cardiac arrest, cerebrovascular disorder; ischaemia; angiogenesis; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy.
                                                                                                                                                                                                                                                             Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder;
528 -----LAPGFDAELIVKNMFTNQDRNGDGKVTAEEFKLXDQEAKHD 568
                                                             173 DSEELKUMLA---ENDKLVEEIFQHEDKDKNGFISHDEF----SGPKHD 214
                                                                                                                                                                                                                                      Novel central nervous system protein #149.
                                                                                                                                                   AAU87239 standard; Protein; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2000; 2000US-0227182.
23-AUG-2000; 2000US-0227009.
30-AUG-2000; 2000US-0228924.
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2000US-0205515
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                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200155318-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                            05-JUN-2002
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                                                                                                                                                                             AAU87239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>1</del>.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 STWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 VFDIEXLELVAGLPEGYMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGK 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 QASLVFDVALLDLHNPKDSISIENKVV------PENCERISQSGDFLTYHYNGT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-LDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIPGSAVLVFDIHVIDFHNPSDSISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLD 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Indels 158; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KSNLVISCLLL-----VAISNSLVRAQDLKVEVISTPEVCEQKSKNGDSLTMHYTGT 54
                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 20883; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 309; DB 22; Length 216; llarity 23.8%; Pred. No. 1.8e-21; Conservative 50; Mismatches 58; Indels 158
                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 20883
                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                    ABB64697 standard; Protein; 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-191637P,
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL08800.
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nes 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AA;
                                                                                                                                                                                                                                             WO200171042-A2
                                                                                                                                                                                     pharmaceutical
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                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
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                                                                                 ABB64697;
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                        RESULT 14
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2000US-0229509.
2000US-0229513.
2000US-0230437.
                                          2000US-0231244.
2000US-0231413.
2000US-0231414.
                                       000US-0231243
                                                                 2000US-0231968
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                05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                     Claim 9; SEQ ID No 757; 837pp; English.
                                                                                                                                                                                                                                             Rosen CA, Barash SC, Ruben SM;
                               2000US-0249216.
2000US-0249217.
2000US-0249218.
                                                                              2000US-0249265.
2000US-0249297.
2000US-0249299.
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2000US-0251856.
2000US-0251868.
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2000US-0251989.
2000US-0251990.
                                                      2000US-0249244.
2000US-0249245.
2000US-0249264.
                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                        2000US-0251988.
2000US-0256719.
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05-JAN-2001; 2001US-0259678.
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                                                                                                                                2000US-0251030
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                                                                                                                        2000US-0250391
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N-PSDB; ABK43569.
                                                                                                      17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
                              17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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08-DEC-2000;
08-DEC-2000;
       17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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08-DEC-2000;
08-DEC-2000;
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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, system disorders e.g. Alzheimer's disease and amylogenesis, nervous system disorders e.g. Alzheimer's disease and cardicolar dimmunodeficiency virus (AIDS) and fundi, ocular disorders e.g. activitable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallargic rhinitis, renal disorders e.g. malignancies, crespiratory disorders e.g. nonallargic rhinitis, renal disorders e.g. ceptides e.g. nonallargic rhinitis, renal disorders e.g. mycoraclial inferation. The polypeptides can also be used to aid wound healing and ceptihelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting call culture of primary tissues, to regenerate tissues and in chemotaxis. The colline, protein, increase or decrease storage capabilities, fat content, lipid, protein,

9.7%; Score 297; DB 22; Length 131; 47.6%; Pred. No. 1.2e-20; ative 22; Mismatches 32; Indels 12; Gaps Query Match
Best Local Similarity 47.68
Matches 60; Conservative

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April 26, 2003, 06:48:54; Search time 14:5233 Seconds (without alignments) 1162.874 Million cell updates/sec
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1 MAFRGWRPPPPPLLLLLLLWV......AEEFKLXDQEAKHDVTLNLA 574
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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No.	Score	Match	Watch Length	8	ID	Description	
1	1750.5	2	581	~	S	1,	
8	1742	57.0	582	N		'n	
3	244.5	8.0	135	н	0	Sequence 20, Appl	
4	242.5	7.9	141	-	US-07-822-966B-6 Se	ģ	
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9	242.5	7.9	142	Ŋ	PCT-US92-03993-7 Se	7,	
7	231.5	7.6	141	~	US-08-803-899-6		
80	230.5	7.5	107	ო	US-08-894-173-69 Se	69	
6	230.5	7.5	107	ო		83	
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11	230.5	7.5	101	4	US-09-398-193-83 Se	83,	
12	230.5	7.5	119	Ŋ		1,	
13	230.5	7.5	120	Н	US-08-336-618-17 Se		
14	230	7.5	104	m		86,	
15	230	7.5	104	4		98	
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19	227.5	7.4	105	ო	4	84	
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22	207	6.8	107	m	US-08-894-173-66 Se	99	
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27	207	6.8	114	Н	US-08-336-618-16 Se	16,	

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1 000 000	US-08-803-83-2	US-08-707-793A-6	US-08-707-792A-6	US-08-707-793A-4	US-08-707-792A-4	US-08-707-793A-5	US-08-707-792A-5	US-08-197-795-2	US-08-336-618-15	PCT-US92-03993-3	PCT-US95-01721-2	US-08-803-899-4	US-09-012-097A-22	US-08-336-618-13	US-08-963-601-1	US-08-744-701-7	US-08-894-173-67	
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Sequence 7, Application US/08989386
Sequence 7, Application US/08989386
Betent No. 588860
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Gorler, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Falo Alto
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: SAFEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastESC for Windows Version 2.0
APPLICATION DATA:
APPLICATION NUMBER: US/08/989,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTĒRISTICS:
LENGTH: 581 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
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; CLONE: 894162
US-08-989-386-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDSISITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVV 426
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                                                                                                   18 PLLLILQTLERGLGRASP-AGAPLE-DVVIERYHIPRACPREVQMGDFVRYHYNGTFEDG 75
                                                                                                                                                                                                                                                                                                                                   256 LILDVHNPKDTVQLETLELPQGCVRRAVAGDFMRYHYNGSLMDGTLFDSSYSRNHTYNTY
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
NUMBER OF SOUTHORES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/989,386
FILING DATE:
CLASSIFICATION:
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Patent No. 5989860
GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 TFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.0%; Score 1742; DB 2; Length 58
Best Local Similarity 56.4%; Pred. No. 1.2e-166;
Matches 326; Conservative 99; Mismatches 131; Indels
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Patent No. 5763590
"GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billing, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PT-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVERTUTO1
CLONE: 2255114
                                                                                                                                                     650-855-0555
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                       TELEPHONE: 650-855-055
TELEFAX: 650-845-4166
PRIOR APPLICATION DATA:
                  APPLICATION NUMBER:
                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-336-618-20
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Sequence 18, Application US/0833618

Sequence 18, Application US/0833618

Sequence 18, Application US/0833618

Sequence 18, Application US/0833618

SETTLE OF INFORMATION:

APPLICANT: Harding, Matthew W.

APPLICANT: Livingston, David J.

APPLICANT: Livingston, David J.

TITLE OF INVENTION: ENCLANTION: ENCATION OF AN Mr. 52,000 FK506 BINDING

TITLE OF INVENTION: CONA.

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSE: Hamilton, Brook, Smith and Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 KDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.9%; Score 242.5; DB 1; Length Best Local Similarity 47.7%; Pred. No. 1.3e-16; Matches 51; Conservative 17; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 GMDEGLLGVCIGEKRXIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 362
                                                                                                                       STATE: DESCRIPTION OF THE PROPERTY: U.S.A.
ZITH: 02110-2804
COUNTRY: U.S.A.
ZITH: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS./2 Model 502 or 55SX
OPERATING SYSTEM: 18M P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/822,966B
FILING DATE: January 17, 1992
ATFORNEY/AGENT INFORMATION:
NAME: FEASER INFORMATION:
NAME: FEASER INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 542-8906
TELEFRAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPRIATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERRESTICS: LENGTH: 141 amino acids TYPE: amino acid STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-822-966B-6
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US-08-336-618-18
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          APPLICANT: Livingston, David J.

TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 YDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNERVSGVIPPNSVLHF 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 135;
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                                                                                                                                                                                                                                                                                     CITY: Lexington

STATE: Massachusetts

CONTRX: U.S.A.

ZUDI: 0.2173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618

FILING DATE: 09-NOV-1994

CLASSIPICATION: 435

PRIOR APPLICATION NUMBER: US/09/3325

FILING DATE: 11-OCT-1991

PRIOR APPLICATION NUMBER: US 07/777,752

FILING DATE: 11-OCT-1991

PRIOR APPLICATION NUMBER: CT//
FILING DATE: 11-OCT-1991

PRIOR APPLICATION NUMBER: CT//
FILING DATE: 09-OCT-1992

ATFONDREY/AGENTINFORMATION:
ANAMER: UP-DEATAILS

ANAMER: 
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Patent No. 5498597
GENERAL INFORMATION:
APPLICANT: Steart L. Schreiber
APPLICANT: Stuart L. Schreiber
APPLICANT: Barbara E. Bierer
TITLE OF INVENTION: FKBP-13, AN FK506-BINDING
TITLE OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPRENCE/DOCKET NUMBER: VPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
   Harding, Matthew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 135 amino acids
amino acid
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; MOLECULE TYPE: protein
US-08-336-618-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 55; Conserva
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125 DVELVDV 131
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US-07-822-966B-6
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257 KDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIP 316
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                                                                                                                                                                                                                                                                                                                                       30 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPPVFSLGTGGQVIK 87
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                                                                                                                                                                             Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: DONAHOE, PATRICIA K.

APPLICANT: WANG, TONGWEN
TITLE OF INVENTION: GELLULAR RESPONSE TO TGF-BETA LIGANDS
TITLE OF INVENTION: GELLULAR RESPONSE TO TGF-BETA LIGANDS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,899
FLING DATE: 02/21/1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/012,054
FLING DATE: 02/22/1996
CLASSIFICATION: 514
                                                                                                                                                                                                   .,3e-16;
nes 36;
                                                                                                                                                                             DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Pred. No. 1.6e-15; 17; Mismatches 37
                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                             7.9%; Score 242.5; 47.7%; Pred. No. 1.3
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NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 0609

TELEPOM (202)371-260

TELEFAK: (202)371-260

TELEFAK: (202)371-260

TELEFAK: (202)371-260

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

TELEFAK: 141 amino arida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-803-899-6; Sequence 6, Application US/08803899; Patent No. 5912224
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TYPE: amino acid
                                                                                                                                                                                                                                       51; Conservative
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                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US92-03993-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear; MOLECULE TYPE: protein US-08-803-899-6
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 51; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 50; Conserva
                      AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLBDGTEFDSSLPQNQPPVFSLGTGGQVIK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application PC/TUS9203993
GENERAL INFORMATION:
APPLICANT: Harding, Matthew W.
TITLE OF INVENTION: RFKERP: A NOVEL PROLYL ISOMERASE AND TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN WHOMER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Leaington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 GMDEGLLGVCIGEKRXIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.9%; Score 242.5; Best Local Similarity 47.7%; Pred. No. 1.3e Matches 51; Conservative 17; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-0CT-1991
PRIOR APPLICATION NUMBER: PCT/
APPLICATION NUMBER: PCT/
FILING DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REFRENCE/DOCKET NUMBER: VP19
TELECOMMULTAAION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 142 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-336-618-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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PCT-US92-03993-7
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STATE: M. COUNTRY:
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                                                                                                                                              TYPE: PRT
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                                                                                                              Sequence 69, Application US/08894173A

Patent No. 6090612

GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
FILE REPREBRICE: P14716C

CURRENT APPLICATION NUMBER: US/08/894,173A

CURRENT FILING DATE: 1997-08-13

NOMPER OF SEQ ID NOS: 97

SEQ ID NO 69
; Sequence 69, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 83, Application US/08894173A
Patent No. 6090612
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
FILE REFERENCE: P14716C
CURRENT APPLICATION NUMBER: US/08/894,173A
CURRENT FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Neurospora crassa
US-08-894-173-69
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ORGANISM: Neurospora crassa
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US-09-398-193-69
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US-08-894-173-83
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7.5%; Score 230.5; DB 4; Length 107;
Best Local Similarity 45.0%; Pred. No. 1.3e-15;
Matches 50; Conservative 14; Mismatches 42; Indels 5
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GENERAL INFORMATION:
APPLICANT: Harding Matthew W.
TITLE OF INVENTION: RFKBP: A NOVEL PROLYL ISOMERASE AND TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-198-13
US-09-198-13
; Sequence 83, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                Query Match 7.5%; Score 230.5; DB 4 Best Local Similarity 45.0%; Pred. No. 1.3e-15; Matches 50; Conservative 14; Mismatches 42
FILE REFERENCE: P24360-
CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 69
LENGTH: 107
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Neurospora crassa
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION UNDRER: 32,227
REFRENCE/DOCKET UNDRER: VPI9:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-861-6240
TELEFAX: 617-861-6540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE GHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
Matches 45; Conserv
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US-08-894-173-86
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US-09-398-193-86
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Patent No. 5763590
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.5%; Score 230.5; DB 5; Length Best Local Similarity 45.0%; Pred. No. 1.6e-15; Matches 50; Conservative 14; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Lexington.
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/336,618
PITING DATE: 09-NOV-1994
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vērsion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
                                                                                                                                                                                                                               NAME: Granaham, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 19,191-05A PCT
TELECOMMUNICATION INFORMATION:
TELEPRAN: (617) 861-6240
INFOREMEPAX: (617) 861-9540
INFOREMEPAX: (617) 861-9540
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                        FILING DATE: 19920507
CLASSIFICATION:
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992
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381 DCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGE 440
                                                                                             31 GSDAELQIERRFVPDECPRTVRSGDFVRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKGQL 90
                                                                                                                          5
                                                                                                                                                                                                                   7.5%; Score 230; DB 3; Length 104; 46.9%; Pred. No. 1.4e-15; rive 16; Mismatches 35; Indels
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j Sequence 86, Application US/08894173A

patent No. 6096612

j GENERAL INFORMATION:

APPLICANT: Medical Research Council

TITLE OF INVENTION: Adenylate cyclase and uses therefor

FILE REFERENCE: 914716C

CURRENT APPLICATION NUMBER: US/08/894,173A

CURRENT FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 86

LENGTH: 104

TYPE: PRT
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; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Ademylate cyclase and uses therefor
; TITLE REFERENCE: P24360-
; CURRENT PILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SCURRENT PARENT New 2.1
; SEQ ID NO 86
; LENGTH: 104
       DB 1;
Query Match 7.5%; Score 210.5; DB 1 Best Local Similarity 45.0%; Pred. No. 1.6e-15; Matches 50; Conservative 14; Mismatches 42
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Search completed: April 26, 2003, 06:49:51 Job time: 15.7733 secs

441 KRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLEL 476
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68 KRKLQIPSSLAYGERGVPGVIPPSADLVFDVELVDV 103

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3054
1 MAFRGWRPPPPPLLLLLLLWV......AEBFKLXDQBAKHDVTLNLA 574
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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	Description	Sequence 6,	Seguence	Sequence	Sequence	Sequence 1692,	Sequence 2, Appl:	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES		US-09-225-502-6	US-09-225-502-8	US-09-225-502-4	US-09-925-297-808	US-09-925-300-1692	US-09-225-502-2	JS-10-006-856A-180	US-10-006-818A-180	-015-393A-180	1-946-374-180	-012-121A-180)-015-869A-180	-978-295A-145	-978-697-145	9-978-192A-145	JS-09-999-832A-145	JS-10-001-054-4	JS-09-978-189-145	US-10-028-072-384
	a	us-0	us-0	us-o	us-0	US-0	us-0	US-10	US-10	US-10	US-09	US-10	US-10	US-09	0S-09	us-09	0S-05	US-10	0S-05	US-10
	DB	10	10	10	2	2	10	σ	φ	σ	σ	σ	σ	6	σ	6	σ	σ	თ	σ
	Query Match Length DB	574	388	441	434	366	336	222	222	222	222	222	222	211	211	211	211	211	211	211
	Query Match	99.8	52.6	45.8	44.3	24.3	24.1	8.8	8.8	8.8	8.8	8.8	8.8	8.4	8.4	8.4	8.4	8.4	8.4	8.4
	Score	3048	1606	1399	1354	743	737	268	268	268	268	268	268	256	256	256	256	256	256	256
	Result No.	-	7	m	4	S	φ	7	- 60	0	10	11	12	13	14	15	16	17	18	19

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상 임	1 MAFRGW 1 MAFRGW	ARPPPPI WRPPPPI		\(\frac{1}{2} \)	MAFRGWRPPPPPLLLILLWYTGQAAPVAGLGSDAELQIERFVPDECPRTVRSGDFVRYH 	REVPDECPRT	VRSGDFVR	XH 60	
	61 YVGTFI 61 YVGTFI	PDGQKFD! PDGQKFD!	SSYDRD SSYDRD	STF STF	YVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNE 	ACVNERRFVR ACVNERRFVR	CI PPKLAYGNE CI PPKLAYGNE	NE 120 	0 0

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LENGTH: 441
US-09-225-502-4
                                                                                                                                                                                          SEQ ID NO 4
                                                                                                                                                                                                                        TYPE: PRT
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241 QASLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYS 300
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98.1%; Pred. No. 8.3e-133;
tive 1; Mismatches 5;
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TITLE OF INVENTION: Human FK506 Binding Proteins
FILE REFERENCE: PF392
                                                                                                                                                                                                                                                               541 MFTNQDRNGDGKVTAEEFKLXDQEAKHDVTLNLA 574
                                                                                                                                                                                                                                                                                  FILE REFERENCE: PF9392
CURRENT APPLICATION NUMBER: US/09/225,502A
CURRENT FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/070,875
PRIOR FILING DATE: 1998-01-09
SEC ID NOS: 8
SOFTWARE: PACENTIN VOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09225502A
Patent No. US20020137127A1
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Best Local Similarity 98.19
Matches 302; Conservative
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US-09-225-502-8
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LENGTH: 388
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US-09-225-502-8
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VIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSIS 372
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; Sequence 808, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; PLIG REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.8%; Score 1399; DB 10;
58.0%; Pred. No. 1.4e-114;
tive 77; Mismatches 102;
                                                                     APPLICANT: Moore et al.
TITLE OF INVENTION: Human FK506 Binding Proteins FILE REFRENCE: PF392
CURRENT APPLICATION NUMBER: US/09/225,502A
CURRENT FILING DATE: 1999-01-06
PRIOR PLING DATE: 1999-01-06
NUMBER OF FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
Sequence 4, Application US/09225502A
Patent No. US20020137127A1
GENERAL INFORMATION:
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Matches 255; Conservative
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US-09-225-502-4
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US-09-925-297-808
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347 AKAGGSRGQEIETTVKPRL 365
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Best Local Similarity 58.1
Matches 140; Conservative
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CRGANISM: Homo sapiens
US-09-225-502-2
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LENGTH: 336
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                                                                                                                                   141 IMNSEDQVQIHTYPKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIG 200
                                                                                                                                                                                            201 WLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLHNPKDSI 260
                                                                                                                                                                                                               261 SIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDE 320
                                                                                                                                                                                                                                                                           GLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISITSHYKP 379
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                                                                                                                                                    EIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFTNQDRNGDGKVTAEBF
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; Sequence 1692, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
    APPLICANT: Craig Rosen,
    APPLICANT: Craig Rosen,
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    FILE REFERENCE: PA101
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR RILING DATE: 1999-03-10
; RIOR FILING DATE: 1999-03-10
; ROFTWARE: PLEADING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PLEADIN Ver. 2.0
; SEQ ID NO 1692
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Best Local Similarity 43.5%; Pred. No. 4e-57;
Matches 165; Conservative 45; Mismatches 91; Indels
                                                                           Length
                                                                                                       Indels
                                                                       Query Match

44.3%; Score 1354; DB 10;
Best Local Similarity 57.5%; Pred. No. 1.3e-110;
Matches 249; Conservative 76; Mismatches 102;
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KLKSDEDEERVHE 432
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 ; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-297-808
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NAME/KEY: SITE
LOCATION: (8)
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US-09-925-300-1692
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184 TLLDGTSFDTSYSKGGTYDTYVGSGWLIKGMDQGLLGMCPGQRRKIIIPPFLAYGEKGYG 243
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                                                                                154 FKPPSCPRTIOVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGM 213
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                          24.1%; Score 737; DB 10; Length 336; 58.1%; Pred. No. 1.2e-56; ive 35; Mismatches 50; Indels 10
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Patent No. US20020137127A1

GENERAL INFORMATION:

APPLICANT MOOFE et al.

TITLE OF INVENTION: Human FK506 Binding Proteins
FILE REFERENCE: PF392

CURRENT FILING DATE: 1999-01-06

PRIOR APPLICATION NUMBER: 60/070,875

PRIOR PELING DATE: 1998-01-09

NUMBER OF SEQ ID NOS: 8

SOSTWARE: PatentIn Ver. 2.1
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US-10-006-818A-180
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LENGTH: 222
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APPLICANT: Pan, James
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PL14
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 477
Prior Applicanton removed - See File Wrapper or Palm
SEQ ID NO 180
FEMALE APPLICANTON NOS: 477
Prior Application removed - See File Wrapper or Palm
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8.8%; Score 268; DB 9; Length 222
Best Local Similarity 31.2%; Pred. No. 9.2e-16;
Matches 64; Conservative 44; Mismatches 77; Indels
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APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Food, Wei-Oiang
APPLICANT: God, Wei-Oiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
                                      Sequence 180, Application US/10006856A Publication No. US20030044841A1 GENERAL INFORMATION:
APPLICANT: Baker, Kevin P. APPLICANT: Bostsein, David APPLICANT: Desnoyers, Luc APPLICANT: Besnoyers, Luc APPLICANT: Eaton, Dan 1.
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Grimaldi, Christopher J.
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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Hillan, Kenneth J.
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Hillan, Kenneth J.
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Paoni, Nicholas F
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ORGANISM: Homo sapiens
RESULT 7
US-10-006-856A-180
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US-10-006-818A-180
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830PIC4
CURRENT APPLICATION NUMBER: US/10/006,818A
CURRENT APPLICATION NUMBER: 2001-12-06
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 477
LENGTH: 222
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8.8%; Score 268; DB 9; Length 222;
Best Local Similarity 31.2%; Pred. No. 9.2e-16;
Watches 64; Conservative 44; Mismatches 77; Indels 20; Gaps
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CURRENT APPLICATION NUMBER: US/10/015,393A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 477
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Fong, Sherman
Gao, Wel-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth J.
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Eaton, Dan 1.
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ORGANISM: Homo sapiens
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US-10-015-393A-180
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Best Local Similarity
Matches 64; Conserv
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PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-15
PRIOR PILING DATE: 1998-09-16
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R FILING DATE: 1998-09-23
R APPLICATION NUMBER: 60/101738
R RILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/101741
R FILING DATE: 1998-09-24
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R APPLICATION NUMBER: 60/100683
R FILING DATE: 1998-09-17
R FILING DATE: 1998-09-17
R FILING DATE: 1998-09-17
R APPLICATION NUMBER: 60/100710
R FILING DATE: 1998-09-17
R FILING DATE: 1998-09-17
R FILING DATE: 1998-09-17
R FILING DATE: 1998-09-17
R APPLICATION NUMBER: 60/100711
R FILING DATE: 1998-09-17
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R APPLICATION NUMBER: 60/100849
R FILING DATE: 1998-09-18
R PILING DATE: 1998-09-18
R FILING DATE: 1998-09-17
R PILING DATE: 1998-09-17
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R FILING DATE: 1998-09-18
R RILING DATE: 1998-09-18
R APPLICATION NUMBER: 60/101279
R FILING DATE: 1998-09-22
R PILING DATE: 1998-09-22
R APPLICATION NUMBER: 60/101471
R FILING DATE: 1998-09-22
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APPLICATION NUMBER: 60/101014
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/101068
FILING DATE: 1998-09-18
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FILING DATE: 1998-09-23
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FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101475
FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101476
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APPLICATION NUMBER: 60/101477
FILING DATE: 1998-09-23
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FILING DATE: 1998-09-24
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, C.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P10.
FILE REFERENCE: P2830P10.
FRIOR APPLICATION NUMBER: 60/098716
FRIOR FILING DATE: 1998-09-01
FRIOR FILING DATE: 1998-09-01
FRIOR FILING DATE: 1998-09-01
FRIOR PELING DATE: 1998-09-01
FRIOR PELING DATE: 1998-09-01
FRIOR PELING DATE: 1998-09-02
FRIOR FILING DATE: 1998-09-02
                                                                                                                                                 484 YMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFT 543
                                                                                                                                                                                 144 ---VIKGPRSIETFKQIDMDNDRQLSKABINLYLQREFEKDERPRDKSYQ-DAVLEDIFK 199
                                           425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDGEVPGSAVLVFDIEXLELVAGLPEG 483
                                                                           APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Food, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddweki, Paul J.
APPLICANT: Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION WUMBER: 60/099642
PRIOR PILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/099741
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099754
FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 180, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                544 NODRNGDGKVTAEEFKLXDQEAKHD 568
                                                                                                                                                                                                                                                                                                   200 KNDHDGDGFISPKEYNVY----QHD 220
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PRIOR APPLICATION NUMBER: 60/099602
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FILING DATE: 1998-09-02
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PRIOR FILING DATE: 1998-09-09
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PRIOR PILING DATE: 1998-09-09
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Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan, James
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64; Conservative
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APPLICANT:
APPLICANT:
Matches
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Pred. No. 9.2e-16;
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A PPLICATION NUMBER: 60/102684

R FILING DATE: 1998-10-01

R FILING DATE: 1998-10-01

R FILING DATE: 1998-10-01

R PILING DATE: 1998-10-01
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A APPLICATION NUMBER: 60/103258
R FILING DATE: 1998-10-06
R FILING DATE: 1998-10-07
R FILING DATE: 1998-10-07
R PILING DATE: 1998-10-07
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FILING DATE: 1998-10-07
FILING DATE: 1998-10-07
APPLICATION NUMBER: 60/103395
                                                                                    APPLICATION NUMBER: 60/102240
FILING DATE: 1998-09-29
APPLICATION NUMBER: 60/102307
FILING DATE: 1998-09-29
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FILING DATE: 1998-09-29
APPLICATION NUMBER: 60/102331
FILING DATE: 1998-09-29
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APPLICATION WUMBER: 60/103449
ELING DATE: 1998-10-06
APPLICATION NUMBER: 60/103633
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APPLICATION NUMBER: 60/103678
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APPLICATION WIMBER: 60/103679
APPLICATION UNMBER: 60/103711
APPLICATION NUMBER: 60/103711
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APPLICATION NUMBER: 60/104987
FILING DATE: 1998-10-20
APPLICATION NUMBER: 60/105000
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APPLICATION NUMBER: 60/105104
FILING DATE: 1998-10-21
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FILING DATE: 1998-10-26
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APPLICATION NUMBER: 60/102487
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APPLICATION NUMBER: 60/102570
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APPLICATION NUMBER: 60/103396
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               APPLICATION NUMBER: 60/101916
FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/102571
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APPLICATION NUMBER: 60/103401
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                                                                       ILING DATE: 1998-09-29
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FILING DATE: 1998-09-24
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Best Local Similarity
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2930PIC20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDGEVPGSAVLVFDIEXLELVAGLPEG 483
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                                                                                                                                                                  425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDGEVPGSAVLVFDIEXLELVAGLPEG 483
                                                                                                                                                                                                   484 YMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFT 543
                                                                                                                                                                                                                                                                                                                  368 SDSISITSHYKPPDCSVLSKKGDYLKYHYNASLL-DGT--LLDSTWNLGKTYNIVLGSGQ 424
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77; Indels 20; Gaps
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8.8%; Score 268; DB 9; Length 222
Best Local Similarity 31.2%; Pred. No. 9.2e-16;
Matches 64; Conservative 44; Mismatches 77; Indels
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NUMBER OF SEQ ID NOS: 477
SEQ ID NO 180
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/012,121A CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Betstein, David
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: For, Sherman
APPLICANT: Goo, Wei-Qiang
APPLICANT: Goodwafi, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 180, Application US/10012121A
Publication No. US20030073810A1
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Hillan, Kenneth J.
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; ORGANISM: Homo maplens
US-10-012-121A-180
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RESULT 12

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APPLICANT: Wood, William I.

TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT APPLICATION NUMBER: 09/91865
RICH REILNG DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR PRIOR DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR PLILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
PRIOR PLILING DATE: 1998-03-11
PRIOR PLILING DATE: 1998-03-11
PRIOR PLILING DATE: 1998-03-11
PRIOR PLILING DATE: 1998-03-12
PRIOR PLILING DATE: 1998-03-12
PRIOR PLILING DATE: 1998-03-12
PRIOR PLILING DATE: 1998-03-13
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RAPLICATION NUMBER: 60/078886

RAPLICATION NUMBER: 60/078886

RAPLICATION NUMBER: 60/078936

RAPLICATION NUMBER: 60/078936

RAPLICATION NUMBER: 60/078910

RAPLICATION NUMBER: 60/078910

RAPLICATION NUMBER: 60/078939

RAPLICATION NUMBER: 60/078939

RAPLICATION NUMBER: 60/079294

RAPLICATION NUMBER: 60/079294

RAPLICATION NUMBER: 60/079664

RAPLICATION NUMBER: 60/079664

RAPLICATION NUMBER: 60/079669

RAPLICATION NUMBER: 60/079669

RAPLICATION NUMBER: 60/079669

RAPLICATION NUMBER: 60/079689

RAPLICATION NUMBER: 60/079788

RAPLICATION NUMBER: 60/079788

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RAPLICATION NUMBER: 60/079788
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RR FILING DATE: 1998-03-30
RR FILING DATE: 1998-03-30
RR FILING DATE: 1998-03-30
RR APPLICATION NUMBER: 60/080105
RR FILING DATE: 1998-03-31
RR APPLICATION NUMBER: 60/080105
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080327
                                                                                                                                                                                                                 Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                                                                                                   Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                        Paoni, Nicholas F.
Kljavin, Ivar J.
                          Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                            APPLICANT
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APPLICANT: Pan, James
APPLICANT: Panni, Names
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERRICE: P2830PLC45
CURRENT APPLICATION NUMBER: US/10/015,869A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 180
LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 YMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 SDSISITSHYKPPDCSVLSKKGDYLKYHYNASLL-DGT--LLDSTWNLGKTYNIVLGSGQ 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAG-VDGEVPGSAVLVFDIEXLELVAGLPEG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 268; DB 9; Length 222; 31.2%; Pred. No. 9.2e-16; tive 44; Mismatches 77; Indels
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US-09-978-295A-145
Sequence 145, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Bacterin, David
APPLICANT: Botterin, David
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                  Application US/10015869A
b. US20030073130A1
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
                                Sequence 180, Application US/10015
Publication No. US20030073130A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bocstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Earon, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong Sherman
APPLICANT: Goo, Wel-Clang
APPLICANT: Goo, Wel-Clang
APPLICANT: Goodard, Audrey
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Baton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 31.2*
Matches 64; Conservative
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US-10-015-869A-180
           US-10-015-869A-180
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APPLICATION WHBER: 60/081071
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081819
APPLICATION DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/081838
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PLICATION NUMBER: 60/082568
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PPLICATION NUMBER: 60/082796
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APPLICATION NUMBER: 60/083336
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APPLICATION WINGBER: 60/083392
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083545
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083500
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APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30
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APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082704
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PLICATION NUMBER: 60/082804
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PLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083554
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APPLICATION NUMBER: 60/080328
                                                                FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081203
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67 HKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEG-KGKIPPESTL 125
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R APPLICATION NUMBER: 60/084639
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
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PLICATION NUMBER: 60/085339
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APPLICATION NUMBER: 60/084643
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RESULT 14
US-09-978-697-145
Sequence 145, Application US/09978697
Sequence 145, Application US/09978697
GENERAL INFORMATION:
APPLICANT: Bakhenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen

APPLICANT: Ferrara, Napoleon APPLICANT: Filvaroff, Ellen APPLICANT: Fong, Sherman APPLICANT: Gao, Wei-Qiang APPLICANT: Gerber, Hanspeter APPLICANT: Gerritsen, Mary E.

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R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083554
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083558
R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/082568
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R APPLICATION NUMBER: 60/082569
R APPLICATION NUMBER: 60/082504
R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/082004
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082700
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R APPLICATION NUMBER: 60/082797
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R APPLICATION NUMBER: 60/08336
R PILING DATE: 1998-04-23
R APPLICATION NUMBER: 60/08332
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R PILING DATE: 1998-04-28
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R FILING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/081195

R APPLICATION NUMBER: 60/081203

R APPLICATION NUMBER: 60/081229

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R APPLICATION NUMBER: 60/081955

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R APPLICATION NUMBER: 60/081819
                    R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080194
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080327
R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080328
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R APPLICATION NUMBER: 60/081070
R PILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/084366
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R PAPLICATION NUMBER: 60/079923
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R APPLICATION NUMBER: 60/080105
R FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079923
                          Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Filvaroff, Ellen
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8.4%; Score 256; DB 9; Length 211;
Best Local Similarity 33.0%; Pred. No. 9.7e-15;
Matches 73; Conservative 38; Mismatches 88; Indels
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Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Faton, Dan
APPLICANT: Ferrara, Napoleon
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RRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/08577
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
                                                                                                                                                                                                                                                                    R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084598

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084600

R FILING DATE: 1998-5-07

R APPLICATION NUMBER: 60/084643

R PILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084643

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/085339

R FILING DATE: 1998-05-13

R APPLICATION NUMBER: 60/085339
                                                                                                    R PILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084637
R FILING DATE: 1998-05-07
R FILING DATE: 1998-05-07
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085700
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APPLICATION WINBER: 60/085689
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
                                                  FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/08441
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                             APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-05
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PRIOR APPLICATION NUMBER: 60/080329
PRIOR PILING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-29
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FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
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67 HKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEG-KGKIPPESTL 125 352 SAVL-VFDIHVIDFHNPSDSISITSHYKPPDCSVLSKKGDYLKYHYNASL-LDGTLLDST 409 468 VFDIEXLELVAGLPEGYMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGK 527 410 --WNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVL 467 22; Query Match 8.4%; Score 256; DB 9; Length 211; Best Local Similarity 33.0%; Pred. No. 9.7e-15; Matches 73; Conservative 38; Mismatches 88; Indels 33; Conservative 38; Mismatches 88; Indels 33; Matches 88; Match PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
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PRIOR PILING DATE: 1998-05-05
PRIOR PELING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084411
PRIOR APPLICATION NUMBER: 60/084411
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PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085502
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PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085503
PRIOR PILING DATE: 1998-05-15
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Gaps

Search completed: April 26, 2003, 07:06:37 Job time : 20.1541 secs

528 LAPGFDAELIVKNMFTNQDRNGDGKVTAEEFKLXDQEAKHD 568

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 26, 2003, 06:48:54; Search time 18.1541 Seconds (without alignments) 3039.596 Million cell updates/sec Run on:

US-09-225-502-6 3054 1 MAFRGWRPPPPPLLLILLLAWV......AEBFKLXDQEAKHDVTLNLA 574 Title: Perfect score: Scoring table: Sequence:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote hypothetical prote	peptidyl-prolyl ci FK506-binding prot peptidyl-prolyl ci	peptidyl-prolyl ci hypothetical prote	peptidylprolyl iso FK 506-binding pro	FK506-inhibitable peptidylprolyl iso	hypothetical prote peptidylprolyl iso	hypothetical prote FKBP-type peptidyl	peptidylprolyl iso
T26537 T21594	T40724 S54139 C82431	D82331 A98277	S56432 JC5764	A40211 A61431	A86118 E82022	T26539 F81245	AF0024
0 0	0 0 0	0 0	0 0	0 0	0 N	20	N
290	112 108 157	259	259 108	105	259 109	108	266
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203.5	196 195.5	184.5	184.5 178	177.5	175.5	173	172.5
30 31	9 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	32 36	37	39	41	43	45

ALIGNMENTS

inding protein - mouse is Mus musculus (house mouse) 12-Jul-1996 #sequence_revision 02-Jul-1996 #text_chang 101. 149669 102. It 4069 103. It 407-409, 1993 104. 407-409, 1993 105. It 407-409, 1993 106. It 407-409, 1993 106. It 406-409 107-108. It 406-409 107-108. It 406-409 108. It 406-409 109. It 406-	173-220/Domain: BKBP-type peptidylprolyl isomerase homology <ppi2> 285-332/Domain: BKBP-type peptidylprolyl isomerase homology <ppi3> 398-445/Domain: BKBP-type peptidylprolyl isomerase homology <ppi4> Query Match 57.3%; Score 1750.5; DB 2; Length 581; Best Local Similarity 58.9%; Pred. No. 3.8e-118; Matches 333; Conservative 90; Mismatches 131; Indels 11; Gaps</ppi4></ppi3></ppi2>	12 PLILILIMVTGQAAPVAGLGSDAELQIERRFVPDECPRTVRSGDFVRYHYVGTFPDG 68	69 OKEDSSYDRDSTENVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNERVSGVIPP 128	129 NSVLHPDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHN 188 :: : : :	189 RMKTYDTYVGIGWLIPGMDKGILGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDV 248 	249 ALLDLANPKOSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLEDSSYSRNRTFDTY 308	309 IGGGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNP 367 	368 SDSISITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVV 426 : : : : : : :
RESULT 1 149669 FRBP65 bd C;Species C;Date: C;Access C;Access R;Simek, Genomics A,Title: A,Referen A,Referen A,Referen A,Referen A,Referen A,Referen A,Referen C;Super C;Super C;Super C;Super C;Super C;Super E;61-108	F; 173 F; 285 F; 398 Oue: Bess	유	ठ _ं व	ç d	& 2	දි සි	දු දු	& g

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A; Gene: CESP: C05C8.3
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A; Introns: 119/3
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NyAlternate names: FK506-binding protein; peptidylprolyl cis-trans isomerase; Pplase
C;Species: Triticum aestivum (common wheat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S5383
R;Oshra, B.; Breiman, A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S5383
A;Reference number: S5383
A;Reference number: S5383
A;Accession: S5383
A;Accession: S5383
A;Molecule type: mRNA
A;Residues: 1-559 <OSH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZpS8610821.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: T42709
S;Accession: T42709
Submitted to the Protein Sequence Database, November 1999
A;Reference number: Z2231
A;Accession: T42709
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-262 <AAA>
A;Residues: 1-262 <AAA>
A;Cscession: Sequence Database, November 1999
C;Accession: T42709
A;Status: preliminary
A;Residues: 1-262 <AAA>
A;Residues: 1-262 <AAA>
A;Cscession: GMBL:AL133116
C;Genetics: GMBL:AL133116
C;Genetics: Capter Capt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 SITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 MGLREMCVGEKRIVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMFIWNG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 EVSPNI FEELDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFTNQDRNGD 550
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427 LGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMF
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C,Superfamily: BKBP-type peptidylprolyl isomerase homology
F,79-126/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 262;
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52.5%; Pred. No. 1.3e-45;
iive 53; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                         547 RNGDGKVTAEEFKL---XDQEAKHD 568
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Best Local Similarity 52.5*
Matches 137; Conservative
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-261 <SAM>
A;Residues: 1-261 <SAM>
A;Cross-references: EMBL:AF016430; PIDN:AAB65370.1; GSPDB:GN00023; CESP:C05C8.3
A;Experimental source: strain Bristol N2; clone C05C8
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A, Eross-references: EMBL:X86903; NID:g854625; PIDN:CAA60505.1; PID:g854626 C; Genetics: FKBP70 C; Superfamily: peptidylprolyl isomerase ROF1; BKBP-type peptidylprolyl isomerase isomerase; cyclosporin A binding C; Superfamily: peptidylprolyl isomerase homology <PPII> F; 60-107/Domain: BKBP-type peptidylprolyl isomerase homology <PPII> F; 293-341/Domain: BKBP-type peptidylprolyl isomerase homology <PPI> F; 293-341/Domain: BKBP-type peptidylprolyl isomerase homology <PPI> F; 293-341/Domain: Extratricopeptide repeat homology <PPI> F; 448-517/Domain: tetratricopeptide repeat homology <PPI
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Cibate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 02-Sep-2000
Ciaccession: T31741
R;Sammons, L.; Wohldmann, P.
submitted to the EmBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C05C8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TİPPELAYGESGSPPTİPANATLQFDVELLSWTSVRDIAKDGGIFKKILKEGDKWENPKD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-----DEVFVKYEARLEDGTVVSKSEG----VEFTVKDGHLCPALAKAVKTMKKGEKV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 ILAVKPQYGFGEMGRPAAGEGGAVPPNASLVIDLELVSWKTVTEIGDDKKILKKVLKEXE 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVRSGDFVRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFV 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%; Score 382; DB 1; Length 559; 30.1%; Pred. No. 1e-19; ive 54; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 KIPPKLAYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.3%; Score 344.5; DB 2;
Best Local Similarity 32.2%; Pred. No. 1.8e-17;
Matches 73; Conservative 51; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C05C8.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.1*
Matches 113; Conservative
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us-09-225-502-6.rpr

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Best Local Sim:
Matches 102;
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                                                                                                                                                                                                                                                                 A;Gene: ROF1
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NyAlternate names: FK506-binding protein; immunophilin; rotamase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S72485; S72484
R;Vucich, V.A.; Gasser, C.S.
R;Vucich, V.A.; Gasser, C.S.
A;Title: Novel structure of a high molecular weight FK506 binding protein from Arabidops
A;Reference number: S72484; MUID:97071666; PMID:8914512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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A;Cross-references: EMBL:U80445; PIDN:AAB37799.1; GSPDB:GN00019; CESP:C50F2.6
A;Experimental source: strain Bristol N2; clone C50F2
                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C50F2.6 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
R,Du, Z.; Le, T.T.
submitted to the EMBL Data Library, November 1996
A,Description: The sequence of C. elegans cosmid C50F2.
                                                                                                            89 IAMEGMCVGEQRKVIIPPEQGFDEDG-DEVEGKGETLYYFVELKSIFRPKPGAKWITDEG 147
                                                                                                                                                                          430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NPKDSISIE--NKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTY 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKD-IPGQASLVFDVALLDLH---- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 WKDEDGLEIKIIRPIKAEKCPIKSQDGDVLDQWYKLSDKDGKEIGSNFNK-KPYTFTLGK 82
                         30 IEIIKKIGDSKCKIKSESGDQLEQFYKLSDKEGKVIGSNFGQ-KPYTFTLGKGEVIHGME
                                                                                                                                                                                                   260 ISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMD
                                                                                                                                                                       371 ISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 75/2; 205/3
A; Introns: 75/2; 205/3
C; Superfamily: BKBP-type peptidylprolyl isomerase homology
F; 50-96/Domain: BKBP-type peptidylprolyl isomerase homology < PPII>
F; 111-218/Domain: BKBP-type peptidylprolyl isomerase homology < PPII>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Indels 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 264;
                                                                                  320 EGLLGVCIGEKRXIVVPPHLGYGEGRGNIPGGA-VLVPDIHVIDFHNP---
                                                                                                                                                                                                                                                                                          431 MGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 11.2%; Score 343; DB 2; 1. Similarity 37.5%; Pred. Np. 2.4e-17; 87; Conservative 36; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Allotrons: 62/1; 91/1; 178/1; 203/1; 230/1; 295/1; 326/1; 384/3; 425/3; 474/3; 517/2, C; Superfamily: peptidylprolyl isomerase ROF1; BKBP-type peptidylprolyl isomerase homc(C; Superfamily: negridylprolyl isomerase homclosy calmodulin binding; cis-trans-isomerase homology cPPII>
C; F27-104/Domain: BKBP-type peptidylprolyl isomerase homology cPPII>
F; 720-339/Domain: BKBP-type peptidylprolyl isomerase homology cPPII>
F; 290-339/Domain: BKBP-type peptidylprolyl isomerase homology cPPII>
F; 449-447/Domain: tetratricopeptide repeat homology cTTI>
F; 449-482/Domain: tetratricopeptide repeat homology cTTI>
F; 482-516/Domain: cetratricopeptide repeat homology cTTI>
F; 483-516/Domain: calmodulin-binding #status predicted
A;Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-551 <VUC>
A;Cross-references: EMBL:US7838; NID:g1373395; PIDN:AAB82062.1; PID:g1373396
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: U49453; NID: g1354206; PIDN: AAB82061.1; PID: g1354207 C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 MDIWNS-EDQVQIHTYFKPPSCPRTIQVS------DFVRYHYNGTFLDGTLFDSSHN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 LK-WDSVXDICKDGGVFK----KILAVGEKWENPKDLDEVLVKFEAKLEDGTVVGKSDG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 LEINLELVSWKTVSE-VTDDNKVV----KKVLKEGDGYERPNEGAVVKVKLIGKLQDGTV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 F-DSSYSRN-RTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYG----EEGRGN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 FLKKGHGENEEPFEFKTDEEQVVDGLDRAVMKMKKGEVALVTIDPEYAFGSNESQQELAV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 GDGASFLKVGEEKEIQQGLKKKLLKEGEGYETPENGDEVEVHYTGTLLDGTKFDSSRDRA 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 RMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKD----IPGQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
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ilarity 25.4%; Pred. No. 1.3e-14;
Conservative 75; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 IPGSAVLVFDIHVIDFHNPSDSISITSHYKPPDCSVLSKKGD 390
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                                                                                                                                                                                                                                                                                                                                  A;Accession: $72484
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-429,'V',431-551 <VUW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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14;

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A,Map position: 4
A;Introns: 43/2; 80/3
C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomeras:
F;45-92/Domain: BKBP-type peptidylprolyl isomerase homology <PPl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rianonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
Ascience 282, 2012-2018, 1998
Ascience and the nematode C. elegans: a platform for investigating bit A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome. wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: E89251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA92994.1; GSPDB:GN00022; CESP:F36H1.1
                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F36H1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T21882
R;Kershaw, J
Submitted to the EMBL Data Library, January 1996
A;Reference number: Z19482
A;Reference: T21882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein ZC455.10 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E89251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 DSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 ISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMD 319
                                                                                                                  148 QIDQIHKIEADKCKKAEAGDKIYQQYVIRLEDNTLVDSSYSRNAPFVFRLRNREVIDGMD
25 DKLQIGVKKRAENCVQKSRKGDQLAMHYTGTLLDGTEFDSSRTRNEEFTFTLGQGNVIKG
                                                                                SITSHYK-PPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 MDEGLLGVCIGEKRXIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVIDFHNPSDSI 371
                                                                                                                                                                                                                        431 MGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.4%; Score 286.5; DB 2;
48.7%; Pred. No. 1.2e-13;
ative 18; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 266.5; DB 2; Pred. No. 6.7e-12; 38; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Residues: 1.139 <WILD
A)Cross-references: BMBL:Z68760; P.
A,Experimental source: clone F36H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.4%;
Matches 69; Conservative 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.7%
Matches 56; Conservative
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A;Molecule type: DNA
A;Residues: 1-241 <STO>
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A, Map position: 5
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                           homolog
             C; Superfamily: peptidylprolyl isomerase ROFI; BKBP-type peptidylprolyl isomerase C; Superfamily: beptidylprolyl isomerase; cyclosporin A binding C; Keywords: calmodulin binding; cis-trans-isomerase; cyclosporin A binding P;54-101/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>P;169-212/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>P;286-334/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>P;482-515/Domain: tetratricopeptide repeat_homology <TRR>
                                                                                                                                                                                                                                                                     11;
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A;Reference number: Z20390
A;Accession: T27586
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-259 <WIL>
A;Residues: EMBL:Z75554; PIDN:CAA99959.2; GSPDB:GN00023; CESP:ZC455.10
A;Experimental source: clone ZC455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 2C455.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407
                                                                                                                                                                                                                                                                                                                                                57 VEVHYTGTLLDGTKFDSSRDRGTPFKFKLEQGQVIKGWDQGIKTWKKGENASLTIPPDLA 116
                                                                                                                                                                                                                                                                                                                                                                                                                      117 YGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPP-----SCPRTIQVSDFV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 GBQGRAATEVEGAVPPNSTLHIDLQLVSWKTLTLIGDDKRILKKVLKGGEGYER-PNDGA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 FLIYHYNGTLLDGTLF-DSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPH 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 VVRVGLIGKLDDGTVFTKKGHEGDEPFEFKTDEEQVIQGLDTTVLTMKKGEEASARIPPE 347
                                                                                                                                                                                                                                                                                                               57 VRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLA 116
                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 TVKYEARLEDGSVVSKS----ESIEFSVKDGYFCPALSKAVKTWKKGEKVLLTVKPQYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEDGDGKD-----IPGQASLVFDVALLD---LHNPKDSISIENKVVP--ENCERISQSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | : | : | : | : 348 HAFGSTETKLSSLIPAVVPPNSSVFYEVELVSFEKEKESWDLKSNSEKIEAASEKKDEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 RYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 LGYGEEGR-----GNIPGSAVLVFDIHVIDFHNPSDSISITSH------YKPPDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 ISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Map position: 5
A, Introns: 27/3; 116/2; 200/3
A, Introns: 27/3; 116/2; 200/3
C, Superfamily: BKBP-type peptidylprolyl isomerase homology
F;52-99/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>F;166-213/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
                                                                                                                                                                                                                                                                     42;
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                                                                                                                                                                                                           Length 568;
                                                                                                                                                                                                                                      ; Pred. No. 2.6e-14;
57; Mismatches 168; Indels
                                                                                                                                                                                                                DB 2;
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C'Date: 15-Oct-1999 #sequence_revision 15-Oct-
C'Accession: 127586
C'hightning, J.
Submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                           10.1%; Score 307;
27.8%; Pred. No. 2
                                                                                                                                                                                                           Query Match
Best Local Similarity 27.8$
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 AWFKMGKYAK 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 VLSKKGDYLK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 72; Conserv
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Gaps

1;

Indels

84

9

33;

87; DB 2;

Length

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isomerase
                            Probable peptidylprolyl isomerase (BC 5.2.1.8) FKBPIS precursor - fava bean NFAlternate names: PK506-binding protein; immunophilin; rapamycin-binding protein Cybecies: Vicia faba (fava bean)
Cybecies: Vicia faba (fava bean)
Cybecies: Vicia faba (fava bean)
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Cybecies: Vicia faba (fava bean)
Cybecies: Vicia faba (fava bean)
Cybecies: Mall, A. 12090
A; Title: Molecular characterization of a FKBP-type immunophilin from higher plants.
A; Accession: T12090
A; Status: preliminary; translated from GB/BMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: Taba>
A; Constructerizations: VID: G1272409; PIDN: AAC49392.1; PID: G1272410
                                                                                                                                                                                                                                                                                                                                                                                                                                        A Gene: FKBP15
A;Note: inhibited by immunosuppressant drugs FK506 and rapamycin
C;Superfamily: BKBP-type peptidylprolyl isomeraes; BKBP-type peptidylprolyl isomeraes; BKBP-type peptidylprolyl isomeraes; immunoregulation
C;Keywords: cis-trans-isomerase; cyclosporin A binding; immunoregulation
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-151/Product: peptidylprolyl isomerase FKBP15 #status predicted <MAT>
F;49-96/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y18D10A.19b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 SSYSRNRIFDIYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGR-GNIPGSAVL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 SSFERNSPIDFELGGGQVIKGWDQGLLGMCLGEKRKLKIPAKLGYGEQGSPPTIPGGATL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 NSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 RMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LIFTIFIIASALVAAKSAADVTELQIGVKYKPASCEVQAHKGDKVKVHYRGKLTDGTVFD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 LVFDV-----ALLDLHNPKD--SISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFD
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A;Residues: 1-304 <WIL>
A;Cross-references: EMBL:AL034393; PIDN:CAA22329.1; CESP:Y18D10A.19b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Gene: CESP:Y18D10A.19b
A/Introns: 82/1; 148/3; 195/1; 262/3
A/Introns: BZBP-type peptidylprolyl isomerase homology
C;Superfamily: BKBP-type peptidylprolyl isomerase homology
F;102-149/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
F;216-263/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.6%; Score 263; DB 2;
42.1%; Pred. No. 6.4e-12;
live 22; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: 220226
A;Accession: T26538
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R,Harris, B.
Submitted to the BMBL Data Library, December 1998
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128 IFDTELVGVNDKS 140
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Best Local S:
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C;Keywords: blocked amino end; cis-trans-isomerase; lipoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: $46228
R,Pahl, A.; Keller,U
EMBO J. 13, 3472-3480, 1994
A;Title: Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting of two A;Reference number: $46227; MUID:94341259; PMID:8062824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptidylprolyl isomerase (EC 5.2.1.8) FKBP-33 precursor - Streptomyces chrysomallus
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F:19-311/Product: peptidylprolyl isomerase homology <PPI1>
F:27-125/Domain: BKBP-type peptidylprolyl isomerase homology <PPI1>
F:224-271/Domain: BKBP-type peptidylprolyl isomerase homology <PPI2>
F:19/Modified site: fatty acylated amino end (Cys) (in mature form) #status F:19/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.Alternate names: fkbB protein
C;Species: Streptomyces chrysomallus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                               430
                                                                                                                                                                                                                           :|: |||
--EVIDGMD 189
                                                                                     371
                                                                                                               BRISOSGDFLTYHYNGTLLDGTL-FDSSYSRNRTFDTYIGOGYVIPGMDEGLLGVCIGEK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414
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A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84280.1; PID:g633644
A;Experimental source: ATCC 11523
|:|::|||||||34 ITITSSIDESECEIKSAGGDVVDQYYKLTDEKGVEIGSNPGK-KPYTFTLGRNQVIPGMD
                                                                                                                                                                                         372 SITSHYK-PPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD
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                                                                               320 BGLLGVCIGEKRXIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFH--NP--
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                                                                                                                                                                                                                                                                                                                                       431 MGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.6%; Score 263.5; DB 1;
27.6%; Pred. No. 1.6e-11;
ve 49; Mismatches 100;
                                                                                                                                                                                                                           148 QIDQIHKIEADKCKKAEAGDKIYQQYVLRLEDNTL.
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A; Molecule type: mRNA
A; Residues: 1-134 < PAN>
A; Residues: 1-134 < PAN>
A; Residues: 1-134 < PAN>
A; Cross-references: EMBL: X76006; NID: 9435470; PIDN: CAA53594.1; PID: 9435471
C; Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase
F; 41-88 Domain: BKBP-type peptidylprolyl isomerase homology < PPI>
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C,Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase
C,Keywords: cis-trans-isomerase
F;52-99/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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A;Reaidues: 1-163 <LUA>
A;Cross-references: EMBL:U52047; NID:g1272407; PIDN:AAC49391.1; PID:g1272408
C;Genetics:
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C;Species: Botryllus schlosseri
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JT0748; S40074
R;Pancer, Z.; Gershon, H.; Rinkevich, B.
Biochem. Biophys. Res. Commun. 197, 973-977, 1993
A;Title: cDNA cloning of a putative protochordate FK506-binding protein.
A;Reference number: JT0748; MUID: 94092189; PMID: 7505578
                                                                                                   249 ALLDLHNPKOSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTY 308
                                                                                                                                                                                                 ----IHHQVDKAG--NGVMPEN-----GQLVQCYIEIKLADCYTSWSNYESQNPIIFK 132
                                                                                                                                                                                                                                                                                                                                                                   368 SDSISITSHYK-----PPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNI 418
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                                                                                                                                                                                                                                                                                                          IGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEG-RGNIPGSAVLVFDHVIDFHNP 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
               82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
52 RMRTFNH------EGMKKHLRDHVVHKK-------SSCEHEKPGKTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 VLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 KIGKGEVIKGWDQGVAQMSVGEKSKLTISADLGYGPRGVPPQIPANATLVFEVELL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.5%; Score 259.5; DB 2; Length 1
Best Local Similarity 48.1%; Pred. No. 1.3e-11;
Matches 50; Conservative 15; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 EGLIGVCIGEKRXIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
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94 RKLKIPSDMGYGDRGSPPKIPGGATLIFDVELL

Search completed: April 26, 2003, 06:50:55 Job time: 20.1541 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 26, 2003, 06:48:55; Search time 10.2323 Seconds (without alignments) 2326.688 Million cell updates/sec Run on:

US-09-225-502-6 3054 1 MAFRGWRPPPPPLLILILLWV.....AREFKLXDQEAKHDVTLNLA 574 Title: Perfect score: Sequence:

112892 segs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Q43207 triticum ae	P45878 mus musculu	P32472 saccharomyc		P26885 homo sapien	0		Q02790 homo sapien		Q13451 h 51 kda fk	Q64378 mus musculu	_		٠.		_	O42123 xenopus lae	m	P56989 neisseria m	Q62658 rattus norv	8	-		-	P44760 haemophilus	P97534 rattus norv		P57599 buchnera ap		P38911 saccharomyc	244	P28725 streptomyce
SUMMARIES	, ai	FKBX_MOUSE	FKB7 WHEAT	FKB2 MOUSE	FKB2 YEAST		FKB2 HUMAN	FKBP_NEUCR	FKB4_RABIT	FKB4_HUMAN	FKB4_MOUSE	FKBS_HUMAN	FKB5 MOUSE	FKBP_YEAST	FKBP_SCHPO		FKB3 ARATH			FKB1_BOVIN	FKBP_NEIMA	FKB1_RAT	FKBP_NEIMB	FKB1_HUMAN	FKBA_ECOLI	FKBB_ECOLI	FKBY HAEIN	FKBB RAT	FKBB HUMAN	FKBA_BUCAI	FKB1 MOUSE	FKB3_YEAST	FKB3_MOUSE	FKBP_STRCH
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	Query Match Length	581	559	140	135	217	141	120	457	458	457	457	456	114	112	108	208	268	107	107	109	107	109	107	270	202	241	101	101	241	107	411	224	124
ع	Query Match	57.3	12.5	8.1	8.0	7.7	7.6	7.5	7.5	7.5	7.3	•	6.9	6.8	6.4	•	6.3	٠.			•		9.9	•	•		•	•	5.5	٠		5.1	5.1	5.0
	Score	· 10	382	246	244.5	234.5	231.5	230.5	228	228	223	217	210.5	207	196	195.5	191	184	178	176	174.5	172.5	172.5	172	171.5	171	171	170	168	167	164	155	154.5	153
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P26684 bos taurus P26623 chlamydia t O46638 oryctolagus Q00688 homo sapien Q06205 saccharomyc P54397 drosophila O74191 schizosacch Q90175 schizosacch C22870 arabidopsis Q927p3 chlamydia m
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PKB3_BOVIN MIP_CHLTR REA3_RABIT PKB3_HABIT PKB4_YEAST PKB4_YEAST PKB4_CANAL PKB4_SCHPO MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU MIP_CHLMU
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222 223 223 222 222 222 222 222 223 223
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153 151 151 151 144.5 143 137.5 135.5
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ALIGNMENTS

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62056 MW;
                                                                                                           riticum aestivum (Wheat)
                                       STANDARD;
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484
559 AA;
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Matches 113; Conserv
                                                                                                                                         NCBI_TaxID=4565;
                                     _FKB7_WHEAT
Q43207;
15-JUL-1998
15-JUL-1998
16-OCT-2001
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SEQUENCE
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REPEAT
REPEAT
                      RESULT 2
FKB7 WHEAT
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                                                                                                                                                                                                                                                                                                                                                                                                 248
                                                                                                                                                                                                                                                                                                                          OKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNERVSGVIPP 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375
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                                                                                                               65 KDA FK506-BINDING PROTEIN (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL).
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                              68
                                                                                   Isomerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation;
Endoplasmic reticulum; Calcium-binding.
                                                                                                                                                                                                                                                                                                     PLLLLLLWV---TGQAAPVAGLGSDAELQIERRFVPDECPRTVRSGDFVRYHYVGTFPDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.3%; Score 1750.5; DB 1; Length 581; Best Local Similarity 58.9%; Pred. No. 3.8e-119; Matches 333; Conservative 90; Mismatches 131; Indels 11;
                                                                                                                       PPIASE, FKBP-TYPE 1.
PPIASE, FKBP-TYPE 2.
PPIASE, FKBP-TYPE 3.
PPIASE, FKBP-TYPE 4.
EF-HAND 7 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
                                                                                                                      PPIASE, FKBP-TYPE
PPIASE, FKBP-TYPE
                                SMART; SM00054; EFH; 2.
PROSITE; PS00453; FKBP PPIASE 1; FALSE NEG-
PROSITE; PS00454; FKBP PPIASE 2; 1.
PROSITE; PS00054; FKBP PPIASE 3; 4.
PROSITE; PS00014; ER TĀRGET; 1.
PROSITE; PS00018; EF HAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNGDGKVTAEEFKL --- XDQEAKHD 568
InterPro; IPR000886; ER_target..
InterPro; IPR001179; FKBP_PPlase.
Pfam; PF00036; efhand; 2.
Pfam; PF00254; FKBP; 4.
                                                                                                                                                                                                                                         64669 MW;
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181
2393
3309
406
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CA BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
70 KDa peptidylprolyl isomerase (RC 5.2.1.8) (Peptidylprolyl cis-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 TPEVGDEVEVHYTGTLIDGKKFDSSRDRDDTFKFKLGQGQVIKGWDQGIKTMKKGENALF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 TIPPELAYGESGSPPTIPANATLOFDVELLSWTSVRDIAKDGGIFKKILKEGDKWENPKD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 TVRSGDFVRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 P-----DEVFVKYEARLEDGTVVSKSEG----VEFTVKDGHLCPALAKAVKTMKKGEKV 225
                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CV. ATIR; TISSUE=Root tip;
OShra B., Breiman A.; Essue=Root tip;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPLASE THAT BINDS CALMODULIN.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMULARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY: CONTAINS 3
FKBP-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 PRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 KIPPKLAYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKP----
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PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 2; 3.
PROSITE; PS50059; FKBP PPIASE 3; 3.
ISOMerase; Rotamase; Repeat; FPR repeat; Heat shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.4.4
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FKBP-TYPE
FKBP-TYPE
559 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPIASE,
PPIASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPIASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X86903; CAA60505.1; -.
HSSP; P27124; IROT.
INTEAFDO; IPR001179; FKBP_PPIASE.
INTEAFDO; IPR001440; TPR.
Pfam; PF00254; FKBP; 3.
Pfam; PF00515; TPR; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R HSSP; P20081; PAT.

R HSSP; P20081; Pkbp2.

R HSSP; P20081; Pkbp2.

R MD; MG: 95542; Pkbp2.

DR InterPro; IPR001179; PkBP_PPIASE.

DR PROSITE; PS00454; PkBP_PPIASE 1; 1.

DR PROSITE; PS0059; PkBP_PPIASE 2; 1.

DR PROSITE; PS0059; PkBP_PPIASE 2; 1.

RM Isomerase; Rotamase; Signal; Endoplasmic reticulum.

TGNAL 22 PROFITIAL.

TGNAL 23 140 PROFITIAL.

TAMP; F4E7PCC7766A0416 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: PPIASES accelerate the folding of proteins. May function as a component of membrane cytoskeletal scaffols.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                      328
                                                                                                                                                                              345 EVALVTIPPEYAYGSTESKQDAIVPPNSTVIYEVELVSFVKDKESWDLNNSEKIEAAGTK 404
220 IITIPPFLAYGE-----DGDGKDIPGQASLVFDVALLD---LHNPKDSISIENKVVP--E 269
                                                                                                               286 GYERPNE-GAVVTVKITGKLQDGTVFLKKGHDEQEPFEFKTDEEAVIEGLDRAVLNMKKG 344
                                                                                                                                                     329 EKRXIVVPPHLGYGE-EGRGN--IPGSAVLVFDIHVIDFHNPSDSISITSH-----YK 378
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (PPiase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=9408790; Pubmed=7505249;
Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,
Burakoff S.J., Dilella A.G.;
Structural organization of the genes encoding human and murine of FKES06-binding protein (FKBP) 13 and comparison to FKBP1.";
Gene 134:271-275(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                          270 NCERISQSGDFLTYHYNGTLLDGTLF-DSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN. SUBUNIT: Interacts with the C-terminal domain of 4.1G. SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED (PROBABLE).
SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        140 AA
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                                                                                                                                                                                                                                  379 PPDCSVLSKKGDYLK 393
                                                                                                                                                                                                                                                                     405 KEEGNALFKSGKYAR 419
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKBP2 OR FKBP13.
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P45878;
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MEDLINE=92366483; PubMed=1380159;
Nielsen J.B., Foor F., Siekerka J.J., Hsu M.J., Ramadan N.,
Morin N., Shafiee A., Dahl A., Brizuela L., Chrebet G.,
Socian K.A., Parent S.A.;
"Yeast FKBP-13 is a membrane-associated FKS06-binding protein encoded by the nonessential gene FKB2.";
                                                      199 IGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLHNPKD 258
                                                                                                             259 SISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGM 318
                           Gaps
                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FKSGO6-binding protein precursor (FKBP-13) (FKBP-15) (Peptidyl-prolyl
cis-trans isomerase) (Ptase) (EC 5.2.1.8).
FFRZ OR FKB2 OR YDR519W OR D9719.24.
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                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetes;
                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93070605; PubMed=1279908;
Partaledis J.A., Fleming M.A., Harding M.W., Berlin V.;
Baccharomyces cerevisiae contains a homolog of human FKBP-13,
membrane-associated FK506/rapamycin binding protein.";
Yeast 8:673-680(1992).
                                                                                                                                                                                   319 DEGLLGVCIGEKRXIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVIDFHNPSD 369
 Length 140;
                           52; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 89:7471-7475(1992).
; Score 246; DB 1;
; Pred. No. 3.6e-11;
25; Mismatches 52;
                                                                                                                                                                                                                                                                    135 AA
                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                (Rel. 27, Created)
(Rel. 27, Last seq
                             59; Conservative
                                                                                                                                                                                                                                                                    STANDARD;
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                              01-OCT-1993
01-OCT-1993
                                                                                                                                                                                                                                                                    YEAST
  Query Match
Best Local
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                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 YDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNERVSGVIPPNSVLHF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential)
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FK506-binding protein precursor (FKBP-21) (Peptidyl-prolyl cistrans isomerase) (PPlase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 244.5; DB 1; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.4e-11;
21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKS06-BINDING PROTEIN.
09CA3F1568D7E4B4 CRC64;
                       EMBL, M90646; AAA34604.1; -
EMBL, M00767; AAA34605.1; -
EMBL, U3307; AAA34605.1; -
PIR, SA6154; A46154.
HSSP; P20081; 11YAT.
SO002927; FKB2
InterPro; 1PR001179; FKBP_PPIASE.
PROSITE; PS00453; FKBP; 11.
PROSITE; PS00454; FKBP_PPIASE 1; 1.
PROSITE; PS00454; FKBP_PPIASE 2; 1.
PROSITE; PS00454; FKBP_PPIASE 2; 1.
PROSITE; PS00454; FKBP_PPIASE 2; 1.
PROSITE; PS00454; FKBP_PPIASE 3; 1.
ISOMETABE; ROUGH PPIASE 3; 1.
PROSITE; PS00454; FKBP PPIASE 3; 1.
PROSITE; PS00454; FKBP PPIASE 3; 1.
PROSITE; PS00454; FKBP PPIASE 3; 1.
PROSITE; PS00454; FKBP PPIASE 3; 1.
PROSITE; PS00454; FKBP PPIASE 3; 1.
PROSITE; PS00454; FKBP PPIASE 3; 1.
PROSITE; PS00454; FKBP PPIASE 3; 1.
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InterPro; IPR001179; FKBP PPIase.
Pfam; PF00254; FKBP; 1.
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15-DEC-1998 (Rel. 37, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 AA; 14487 MW;
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DVELVDV 131
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Matches
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PROSITE; PS00453; FKBP PPIASE 1; FALSE NEG.
PROSITE; PS00454; FKBP PPIASE 2; 1.
PROSITE; PS00059; FKBP PPIASE 3; 1.
PROSITE; PS00014; ER TARGET; 1.
ISOMERASE; Rotamase; Signal; Endoplasmic reticulum; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                             267 VPENCERISQSGDFLTYHYNGTL-LDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UU-1999 (Rel. 38, Last annotation update)
FKS506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (FF 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93112052; PubMed=1281998; Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.; "Chromosomal band assignments of the genes encoding human FKBP12 and
                                                                                                                                                                           FK506-BINDING PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL).
72313067521BCDAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          1;
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WEDLINES=91319747; PubMed=1713687;
Jin Y.-J., Albers M.W., Lane W.S., Bierer B.E., Schreiber S.L.,
Burakoff S.J.;
                                                                                                                                                                                                                                                                                                       217;
                                                                                                                                                                                                                                                                                              ; Score 234.5; DB 1; Length
; Pred. No. 4.2e-10;
15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of a membrane-associated human FK506-rapamycin-binding protein, FKBP-13.", Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 CIGEKRXIVVPPHLGYGEEGRGNIPGSAVLVFDIHVI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 CIGEKRILIVPPSYGYGQRSIGPIPAGSTLIFETELI 126
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                                                                                                                                                                                                                                    217 AA; 22915 MW;
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EMBL; M75099; AAA36563.1; -.
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                                                                                                                                                                                                                                                                                                                                                       45; Conservative
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Homo sapiens (Human)
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P26885;
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                           CHAIN
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Query Match
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                                                                                                                                                                                                            ;;
(7)
                                                                                                                                                                                                                            257 KDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90348972; PubMed=1696687; Tropschug M., Wachter E., Mayer S., Schoenbrunner E.R., Schmid F.X.; "Isolation and sequence of an FK506-binding protein from N. crassa which catalyses protein folding."; Nature 346:674-677(1990).
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                        29 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 14, Last annotation update)
FKS06-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase)
(Ppiase) (RC 5.2.1.8).
                                                                                                     (POTENTIAL)
                     Min, 100710, 1.
InterPro; IPR01179; FKBP_PPIase.
Pfam; PP0024; FKBP; 1.
PROSITE; PS00453; FKBP_PPIASE_1; 1.
PROSITE; PS00454; FKBP_PPIASE_2; 1.
PROSITE; PS0059; FKBP_PPIASE_3; 1.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
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Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                     ; Score 231.5; DB 1; Length 141; 
; Pred. No. 4e-10; 
17; Mismartches 37; Indels 3;
                                                                                                                                                                                                                                                                 317 GMDEGLLGVCIGEKRXIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 362
                                                                                                                                                                                                                                                                            PREVENT SECRETION FROM ER
                                                                                                                                                           /FTId=VAR 006412.
9F4751CA7D82D064 CRC64;
                                                                                           FK506-BINDING PROTEIN
                                                                                                                    FTId=VAR_006410.
                                                                                                                                r -> A.
/FTId=VAR_006411.
                                                                                                                                                                                                                                                                                                                                     120 AA
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                                                                                                                                                                       15654 MW;
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                                                                                                                                                                                                Local Similarity 46.7 es 50; Conservative
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       HGNC:3718; FKBP2.
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000688;
                 MIM; 186946;
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                                                                                                                                                                     SEQUENCE
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
185-OC-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase FKB96-binding protein) (RPPase) (Roramase) (RC 5.2.1.8) (PPiase) (Roramase) (BC 5.2.1.8) (FKB952 protein) (452 kDa FK506 binding protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 GSDAELQIERRFVPDECPRTVRSGDFVRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKGQL 90
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J. Biol. Chem. 267:4281-4284(1992).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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Miyata Y., Chambraud B., Radanyi C., Leclerc J., Lebeau M.-C.,
Renoir J.-M., Shirai R., Catelli M.-G., Yahara I., Baulieu E.-E.;
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Lebeau M.-C., Massol N., Herrick J., Faber L.E., Renoir J.-M.,
Radanyi C., Baulieu E.-E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 7.5%; Score 230.5; DB 1; Length 120;
1 Similarity 45.0%; Pred. No. 3.9e-10;
50; Conservative 14; Mismatches 42; Indels 5
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Deshpande K.L., Seubert P.H., Tillman D.M., Farkas W.R., K
Cloning and characterization of cDNA encoding the rabbit
tRNA-guanine transglycosylase 60-kilodalton subunit.";
Arch. Biochem. Biophys. 326:1-7(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13037 MW; AF97183C041563B7 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 89:6270-6274(1992).
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STRAIN-New Zealand white; TISSUE-Liver;
or send an email to license@isb-sib.ch)
                                                                                                                                                             EMEL, AL511463, CAC28766.1; -. PIR; S11090; S11090. HSD9. HSD9. FIRD. HSDP. PID303; JFKL. INTERPROPERS. J. PROSITE; PS00453; FKBP_PPIASE. PROSITE; PS00454; FKBP_PPIASE. J. PROSITE; PS00454; FKBP_PPIASE. J. PROSITE; PS00454; FKBP_PPIASE. J. J. PROSITE; PS0059; FKBP_PPIASE. J. J. PRO
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01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                 EMBL; X55743; CAA39274.1;
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P27124;
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                                                                                                                                                                                                                                                                                                                  TRUCTURE BY NWR OF 1-148.

WEDLINE=96374215; PubMed=8780506;
A Craescu CT., Rouviere N., Popescu A., Cerpolini E., Lebeau M.-C.,
A Bauliau E.-E., Mispelter J.;
FREPS in solution.";
RI FREPS in solution.";
RI Biochemistry 35:11045-11052(1996).
CC Complexes that sediment at 8-10 S. May have a rotamase activity.
CC May play a role in the intracellular trafficking of heteroligoneric forms of steroid hormone receptors.
CC CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC CC PERTIDE BONDS IN OLIGOPEPTIDES.
CC PERTIDE ASSOCIATES With HSP90 and HSP70 in unactivated steroid CC CONTRACTIVITY: ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASSOCIATES ASS
"Phosphorylation of the immunosuppressant FK506-binding protein FKBP52 by casein kinase II: regulation of HSP90-binding activity of FKBP52."; Proc. Natl. Acad. Sci. U.S.A. 94:14500-14505 (1997).
                                                                                                INTERACTION WITH PHYH.
MEDLINE-99162565; PubMed-10051602;
Chambraud B., Radanyi C., Camonis J.H., Rajkowski K., Schumacher M.,
                                                                                                                                                                                                    "Immunophilins, refsum disease, and lupus nephritis: the peroxisomal enzyme phytanoyl-COA alpha-hydroxylase is a new FKBP-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hormone receptor complexes. Also interacts with peroxisomal phytanoyl-coA alpha-hydroxylase (PHYH) (By similarity).
--- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
--- PTM: Phosphorylation by CK2 results in loss of HSP90 binding
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PROSITE; PS00453; FKBP_PPIASE_1; 1.
PROSITE; PS00454; FKBP_PPIASE_2; 2.
PROSITE; PS50059; FKBP_PPIASE_3; 2.
ISOMerase; Rotamase; TPR repeat; Repeat; Nuclear protein;
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-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
-!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.
-!- SIMILARITY: CONTAINS 3 TPR REPEATS.
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TPR 2.
TPR 3.
PHOSPHORYLATION (BY CK2)
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                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 96:2104-2109(1999).
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FKBP-TYPE
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PPIASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; IROT; 07-DEC-96.
PDB; IROU; 07-DEC-96.
InterPro; IRROU119; FKBP_PPIase.
InterPro; IRROU1440; TPR.
Pfam; PF00254; FKBP; 2.
Pfam; PF00515; TPR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SG 'S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M84474; AAA31438.1; -. EMBL; M84988; AAA31439.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
20
25
457 AA;
                                                                                                                                                                            Baulieu E.-E.;
"Immunophilins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity
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DOMAIN
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CONFLICT
SEQUENCE
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Gaps

28;

27.5%;

Local Similarity

77; Conservative

Matches

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Q02730; Q9UCV7, Q9UCP1;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
FKSO6-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase
FKBP4) (RC 5.2.1.8) (PPiase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peattie D.A., Harding M.W., Fleming M.A., Decenzo M.T.,
Lippke J.A., Livingston D.J., Benasutti M.,
"Expression and characterization of human FKBP52, an immunophilin
that associates with the 90-kDa heat shock protein and is a component
                                                                                                                                           253
                                                                                                                                                                                                                                                                                HNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDT----Y 308
                                                                                                                                                                                                                                                                                                                                                  TDDEDGGII------RRIRTRGEGYARPNDGAIVEVAL--EGYYKDRLFDQRELRFE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:| : |:::|: | | | | | :::|:
191 VGEGESLDLPCGLEKAIQRMEKGEHSILYLKPSYAFGNAGKEKFQIPPYAELKYEVHLKS 250
MDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVG 198
                                                                                                                                                                                                                                                                                                                                                                                                                        309 IGQGYVIP---GMDEGLLGVCIGEKRXIVVPPHLGYGEEGRG--NIPGSAVLVFDIHVID 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tai P.-K.K., Albers M.W., Chang H., Faber L.E., Schreiber S.L.;
"Association of a 59-kilodalton immunophilin with the glucocorticoid
recentor complex.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-0035521; PubMed=2378870; Sanchez E.R., Faber L.E., Henzel W.J., Fratt W.B.; Faber L.E., Henzel W.J., Fratt W.B.; The 56-59-46110dalton protein identified in untransformed steroid receptor complexes is a unique protein that exists in cytosol in a Ecomplex with both the 70- and 90-kilodalton heat shock proteins."; Biochemistry 29:5145-5152 (1990).
                                                   22 VDISPKQDEGVLKVIKREGTGTETPMIGDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDLG
                                                                                                                                                                                IGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALL----DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo, sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-20, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung, Lymph, and Uterus;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 89:10974-10978(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 FHNPSDSISITSHYKPPDCSVLSKKGD-YLKY-HYNASLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92285692; PubMed=1376003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
MEDLINE=93066366; PubMed=1279700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of steroid receptor complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 256:1315-1318(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lymphocytes;
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TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor complex.
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139
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SEQUENCE FROM N.A.
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                                                                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 YDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNERVSGVIPPNSVLHF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVLLM-----DIWNSED-----QVQIHTYFKPPSCPRIIQVSDFVRYHYNGTFLDGTL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 OSAPLPMEGVDISPKODEGVLKVİKREGTGTEMPMI---GDRVFVHYTGWLLDGTKFDSS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAAPVAGLGSDAELQ-----IERRFVPDECPRTVRSGDFVRYHYVGTFPDGQKFDSS 74
                                  -!- PTM: Phosphorylation by CK2 results in loss of HSP90 binding activity (By similarity).
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
-!- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOWAINS.
-!- SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                          hormone receptor complexes. Also interacts with peroxisomal phytanoyl-coA alpha-hydroxylase (PHYH).
SUBCELLUIAR LOCATION: MUCLear and cytoplasmic.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY CK2) (BY S:
ED -> AR (IN REF. 2; AAH02887)
916B3B945C51634E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 458;
      Yem A.W., Tomasselli A.G., Heinrikson R.L., Zurcher-Neely H. Ruff V.A., Johnson R.A., Deibel M.R. Jr.; "The Hsp56 component of steroid receptor complexes binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.5%; Score 228; DB 1; Length 458 29.7%; Pred. No. 3.2e-09; ive 35; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00028; TPR; 3.
PROSITE: PS00453; FKBP_PPIASE 1; 1.
PROSITE: PS00454; FKBP_PPIASE 2; 2.
PROSITE; PS0059; FKBP_PPIASE 3; 2.
ISOMERASE; REQUART REPEASE 3; 2.
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FKBP-TYPE
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PPIASE,
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TPR 2.
TPR 3.
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Interpro; IPRO01444; PPR._
Pfam; PF00254; FKBP; 2.
Pfam; PF00515; TPR; 3.
 MEDLINE=92147620; PubMed=1371107;
                                                                                                                                                                                                                                                                                                   EMBL; M88279; AAA36111.1; -.
EMBL; BC001786; AAH01786.1; -.
EMBL; BC005887; AAH02887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51673 MW;
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PIR; A46372; A46372.
HSSP; P27124; 1ROT.
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269
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458 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation.
INIT_MET 0
DOMAIN 49
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CONFLICT
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REPEAT
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P305<u>T7 AA.</u>
P306<u>T6;</u>
P306<u>T6;</u>
P306<u>T7 AA.</u>
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                                                                                                                                                                                                                                                                                   PDQRELRFE-----IGEGENLDLPYGLERAIQRMEKGEHSIVYLKPSYAFGSVGKEKFQ1 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alnemri B.S., Fernandes-Alnemri T., Nelki D.S., Dudley K., Dubbols G.C., Litwack G.; "Overexpression, characterization, and purification of a recombinant mouse immunophilin FKBP-52 and identification of an associated
EVELFEFKGEDLTEEEDGGIIRRIQTRGEGYAKP-----NEGAIVEVALEGYYKD-KL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Component of unactivated mammalian steroid receptor complexes that sediment at 8-10 S. May have a rotamase activity. May play a role in the intracellular trafficking of heterolologometric forms of steroid hormone receptors.

CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
SUBUNIT: ASSOCIATES With HSP90 and HSP70 in unactivated steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormone receptor complexes. Also interacts with peroxisomal phytanoyl-coA alpha-hydroxylase (PHYH) (By similarity). SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Prosphorylation by CK2 results in loss of HSP90 binding activity (By similarity). SIMILARITY: CONTAINS 2 FREP-TYPE PPIASE FAMILY. SIMILARITY: CONTAINS 2 FREP-TYPE PPIASE DOMAINS. SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                                         FDSSHNRMKTYDTYVGIGW---LIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGK-DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 5-457 FROM N.A., PARTIAL SEQUENCE, FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lung tumor;
Strausberg R.;
Submitted (FEE-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphoprotein.";
Proc. Natl. Acad. Sci. U.S.A. 90:6839-6843(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 PPNAELKYELHLKSFEKAKESWEMNSE-----EKLEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 PGQASLVFDVALLDLHNPKDSISIENKVVPENCERISOS
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MEDLINE=94040772; Pubmed=7693550;
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STRAIN=C57BL/6J; TISSUE=Testis;
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                   PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                          139 MDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVG 198
                                                                                                                                                                                                                                                                                                                                                                                                                    253
                                                                                                                                                                                                                                                                                                                                                                                                                                     82 KGEVIKAWDIAVATWKVGEVCHITCKPEYAYGAAGSPPKIPPNATLVFEVELFEFKGEDL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 HNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDT----Y 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 IGQGYVIP---GMDEGLLGVCIGEKRXIVVPPHLGYGEEG--RGNIPGSAVLVFDIHVID 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                                                                     TRGEGYAR -> LGVKAMQG (IN REF. 3).
GLEEAIORMEKGEHSIVYLKPSYAFGSVGKERFQIPPH
AWRRPFSAWRKESIPSCTSNLAMLLAVWGRRGSRSHRT
                                                                                                                                                                                                                                                                                                                                                                                              22 VDISPKODEGVLKVIKREGTGTETPMIGDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDLG
                                                                                                                                                                                                                                                                                                                                                                                                                  199 IGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALL----DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last aequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
51 kDa FK506-binding protein (FKBPS1) (Peptidyl-prolyl cis-trans isomerase) (EC 5.2.1.8) (Ppiase) (Rotamase) (54 kDa progesterone receptor-associated immunophilin) (FKBPS4) (FF1 antigen)
1818-190-binding immunophilin) (Androgen-regulated protein 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            271 EKLEGSNI -> RSWSRATY (IN REF. 3).
314 H -> R (IN REF. 2).
51441 MW; 0D087C543541C1C0 CRC64;
                                                                                                                                                                                                                                                                                                                                     Length 457;
                                                                                                           SMART; SM00028; TPR; 3.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 2; 2.
PROSITE; PS00059; FKBP PPIASE 3; 2.
ISOMERASE; ROLAMASE; REPEAT; TPR repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                   Match 7.3%; Score 223; DB 1; Length 45 Local Similarity 27.9%; Pred. No. 7.3e-09; es 78; Conservative 45; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 FEKAKESWEMSSAEKLEQSNIVKERGTAYFKEGKYKQALL 290
                                                                                                                                                                                FKBP-TYPE 1. FKBP-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 FHNPSDSISITSHYKPPDCSVLSKKGD-YLKY-HYNASLL 401
                                                                                                                                                                                                                                            (IN REF.
                                                                                                                                                                      BY SIMILARITY.
PPIASE, FKBP-TY
PPIASE, FKBP-TY
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                                                                                                                                                                                                                                                                                   (IN REF. 3)
EKLEQSNI -->
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TRGEGYAR
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                                       X17068; CAA34914.1; ALT_SEQ.
                                               HSSP; P27124; IROT.
MGD; MGI:95543; Fkbp4.
InterPro; IPR001179; FKBP PPIASE.
InterPro; IPR001440; TPR.
Pfam; PF00254; FKBP; 2.
Pfam; PF00515; TPR; 3.
                   BC003447; AAH03447.1; -. X17069; CAC39452.1; -.
         EMBL; X70887; CAA50231.1; -.
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137
252
302
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314
457 AA;
                                                                                                                                                             Phosphorylation.
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CONFLICT
SEQUENCE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               Zhang J.S., Smith D.I.; "Identification of AIG6 as an androgen response gene in human prostate cancer cell line LNCaP."; Cancer cell line LNCaP."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94043261; PubMed=7693698;
Smith D.F., Albers M.W., Schreiber S.L., Leach K.L., Deibel M.R. Jr.,
"FKBP54, a novel FK506-binding protein in avian progesterone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- ENZYME REGULATION: INHIBITED BY FK506 BUT NOT CYCLOSPORIN.
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- TISSUB SPECIFICITY: WIDELY EXPRESSED, ENRICHED IN TESTIS COMPARED
                                                                                                      Baughman G., Wiederrecht G.J., Chang F., Martin M.M., Bourgeois S.; "Tissue distribution and abundance of human FREP51, an FK506-binding protein that can mediate caloneurin inhibition."; Blophys. Res. Commun. 232:437-443(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 9-457 FROM N.A.

BULDILINES-97154494; PubMed=9001212;
Nair S.C., Rimerman R.A., Toran E.J., Chen S., Prapapanich V.,
Butts R.N., Smith D.F.;
Modlecular cloning of human FRBP51 and comparisons of immunophilin interactions with Hsp90 and progesterone receptor.";
Mol. Cell. Biol. 17:594-603(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complexes and Hela extracts.";
J. Biol. Chem. 268:24270-24273(1993).
-!- FUNCTION: INTERACTS WITH FUNCTIONALLY MATURE HETERO-OLIGOMERIC PROGESTERONE RECEPTOR COMPLEXES ALONG WITH HSP90 AND P23.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- INDUCTION: By androgen.
-1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0453; FKBP PPIASE 1; 1.
PROSITE; PSO0454; FKBP PPIASE 2; 1.
PROSITE; PS50059; FKBP PPIASE 3; 1.
ISOMETABE; Rytamase; TFR repeat; Repeat; Nuclear protein.
DOMAIN 157 243 PPIASE, FKBP-TYPE 1.
PPIASE, FKBP-TYPE 2.
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SIMILARITY: CONTAINS 3 TPR REPEATS.
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TPR 2.
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InterPro; IPR001179; FKBP_PPlase.
InterPro; IPR001440; TPR.
Pfam; PF00254; FKBP; 2.
Pfam; PF00515; TPR; 2.
                                                                        MEDLINE=97242207; PubMed=9125197;
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317
352
457 AA;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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7.1%; Score 217; DB 1; Length 457;

Query Match

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[1]
SEQUENCE FROM N.A.
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-! FUNCTION: INTERACTS WITH PROGESTERONE RECEPTOR (BY SIMILARITY).

-! CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC

-! CATALYTIC ACTIVITY: OF PROGESTERONE SECTION OF PROLINE IMIDIC

-! ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.

-! SUBCELLULAR LOCATION: Nuclear and CYLODJASMIC.

-! TISSUE SPECIFICITY: WILDELY EXPRESSED, HIGHEST LEVELS FOUND IN THE

-! LIVER, SKELETAL MUSCLE, KIDNEY AND THYMUS. EXPRESSION IS REGULATED
                                                                                                                                                                                                                                                                      256
                                                                                                                                                                                                                                                                                                                                                                                                                      427
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                                                                                                                                                     259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 WEMDTKEKLEQAAIVKEKGTVYFKG-------GKYMQAVIQYGKIVSWL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMFI 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 -----LYRRGEAQLLMNEFE-----SAKGDFEKVLEVNPONKAARLQISM 393
                                                                DIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGI 199
                                                                                                                                                                                                                                          260 ISIENKVVPENCERISQ-----SGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGOGY 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "FKB\overline{\rm P}51, a novel T-cell-specific immunophilin capable of calcineurin inhibition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96074651; PubMed=7479941;
Yeh W.-C., Li T.-K., Bierer B.E., McKnight S.L.;
Tidentification and characterization of an immunophilin expressed during the clonal expansion phase of adipocyte differentiation.";
Proc. Natl. Acad. Sci. U.S.A. 92:11081-11085 (1995).
                                                                                         GWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLHNPKDS
                                                                                                                                                                                                                                                                                                                                                           197 DIPIGIDKALEKMOREEQCILYLGPRYGFGEAGKPKFGIEPNAELIYEVTLKSFEKAKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                              314 VIP-GMDEGLLGVCIGEKRXIVVPPHLGYGEEGRG--NIPGSAVLVFDIHVIDFHNPSDS
                                                                                                                                                                                                                                                                                                                                                                                                                      371 ISITSHYKPPDCSVLSKKGD-YLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVV--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
15-DATE (Rel. 40, Last annotation update)
15-DATE (Respective of Properior (Repsist) (Reprint)
15-DATE (Respective of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of Properior of 
                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 EMEYGLSEKESKASESFLLAAFLNLAMCYLKLREYTKAVECCD-KALGLDSANEKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c; TISSUE-Thymus;
MEDLINE=95349606; PubMed=7542743;
Baughman G., Wiederrecht G.J., Campbell N.F., Martin M.M.,
                         201; Indels
2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AA
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537 IVKNMFTNQDRNGDGKVTAEEF-KLXDQEAKHD 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 COKKAKEHNER--DRRIYANMFKKFAEODAKEE 424
  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                         72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
  23.0%;
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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064378;
                                                                       140
                                                                                                              24
                                                                                                                                                          200
                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 LTYHYNGTLIDGTLFDSSYSRNRTFDTYIGOGYVIP-GMDEGLLGVCIGEKRXIVVPPHL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 LAYGEDGDGKDIPGQASLVFDVALLDLHNPKDSISIENKVVPENCERISQ-----SGDF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 VKVHLEG-CCGGRTFD---CRDVVFVVGEGEDHDIPIGIDKALVKMQREEQCILYLGPRY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYGEEGRG--NIPGSAVLVFDIHVIDFHNPSDSISITSHYKPPDCSVLSKKGD-YLKYHY 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 GFGEAGKPKFGIDPNAELMYEVTLKSFEKAKESWEMDTKEKLTQAAIVKEKGTVYFKG-- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 DEVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                    PPIASE FAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at; Repeat; Nuclear protein.
PPIASE, FKBP-TYPE 1.
PPIASE, FKBP-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FBE-1991 (Rel. 17, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans:
(Ppiase) (BC 5.2.1.8) (Rapamycin-binding protein).
FRRI OR FKB1 OR YBL135C OR N1213 OR N1845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8FD0C9B61478EB46 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.9%; Score 210.5; DB 1
7.8%; Pred. No. 5.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 NASLLDGTLLDSTWNLGKTYNIVLGSGQVV--LGMDMGLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
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                 BELONGS TO THE FKBP-TYPE
                                                                             -!- SIMILARITY: CONTAINS 3 TPR REPEATS
ADIPOCYTE DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00115; TPR; 2.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 2; 1.
PROSITE; PS50059; FKBP PPIASE 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPR 1.
TPR 2.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U16959; AAA86983.1; -.
HSSP; P27124; IRC.
HSD; MGI:104670; FKbp5.
INTERPO; IPR001179; FKBP.
INTERPO; IPR001440; TPR.
PP00054; FKBP; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   somerase; Rotamase; TPR repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50966 MW;
                                                                                                                                                                                                                                                                                                                                                                    EMBL; U36220; AAA89162.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78; Conservative
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                             SIMILARITY: BELONG
FKBP-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 3
456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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PIR; S13758; S13758

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=9316714; Dubmed=75 ANGELOGY.

Retonda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;

Retonda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;

Rotonda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;

Rotonda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;

Crystallographic and functional analysis.";

J. Biol. Chem. 268:7607-7609(1993).

-!- FORTION: PRIABSE ACCELERATE THE FOLDING OF PROTEINS.

-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLICOPEPTIDES.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIBCELLANEOUS: FKEP BINDS TO THE IMUNOSUPPRESSANT DRUG FK506 AND ALSO MEDIATES THE SENSITIVITY TO RAPAMYCIN.

-!- SIMILARITY: BELONGS TO THE FKEP-TYPE PPIASE FAMILY.
                                                                "FKB1 encodes a nonessential FK 506-binding protein in Saccharomyces cerevisiae and contains regions suggesting homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siekierka J.J., Widerrecht G., Greulich H., Boulton D., Hung S.H.Y., Cryan J., Hodges P.J., Slgal N.H., "The cytosolic-binding protein for the immunosuppressant FK-506 is both a ubiquitous and highly conserved peptidyl-prolyl cis-trans lsomerase."
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91141524; PubMed=1996117;
KOLTIN Y., Faucette L., Bergsma D.J., Levy M.A., Cafferkey R.,
KOLTIN Y., Johnson R.K., Livi G.P.;
KOBER P.L., Johnson R.K., Livi G.P.;
"Rapamycin sensitivity in Saccharomyces cerevisiae is mediated by a
Peptidyl-prolyl cis-trans isomerase related to human FK506-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
"BP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                   AEQUENCE FROM N.A.
MEDLINE=91156723; Pubmed=1705713;
Heituan J., Movva R.N., Hiestand P.C., Hall M.N.;
Heituan J., Movva R.N., Piestand P.C., Hall M.N.;
FWE 506-binding protein proline rotamage is a target for the immunosuppressive agent FK 506 in Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 88:1948-1952(1991).
MEDLINE=91126049; PubMed=1704127;
Wiederrecht G.J., Brizuela L., Elliston K.O., Sigal N.H.,
Siekierka J.J.;
                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 88:1029-1033(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 265:21011-21015(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      procein.";
Wol. Cell. Biol. 11:1718-1723(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91065908; PubMed=1701173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96109932; PubMed=8619318;
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A39122.
C38333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
                                                                                                             cyclophilins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A33146; PIR; A37870; PIR; A39122; PIR; C38333; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C;
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41 REVPDECPRIVESGDEVRYHYVGIFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1002 (Rel. 41, Last annotation update)
FKS06-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase)
(PPiase) (EC 5.2.1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 207; DB 1; Length 114;
13.6%; Pred. No. 1.8e-08;
ve 13; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12158 MW; 65C134830D300C06 CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LSVGEKARLTIPGPYAYGPRGFPGLIPPNSTLVFDVELLKV 113
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                     PDB; IYAT; 31-OCT-93.
SGD; S0005079; FRR1.
IIICENTEV; IPRO1179; FKBP PPIASE.
Ffam; PF00154; FKBP; 1.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 1; 1.
PROSITE; PS50059; FKBP PPIASE 2; 1.
ISOMETASE; ROTAMASE; 1.
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Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Meltjens I., Vanstreels E., Reger M., Schaefer M., Mueller-Auer S.,

A Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Berr P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

A Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

A Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

"The genome sequence of Schizosaccharomyces pombe.",

Nature 415: 871-880 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Ilnsecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- MISCELLANEOUS: FKEP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506.
-!- SIMILARITY: BELONGS TO THE FKEP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
12 kDa FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase) (PPIsee) (RC 5.2.1.8) (Macrolide binding protein).
                                                                                                                                                                                                                                                                                            -! - FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%; Score 196; DB 1; Length 11
45.6%; Pred. No. 1.1e-07;
tive 12; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               somerase; Rotamase.
:ROUENCE 112 AA; 12043 MW; 355944ECB84D2539 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001179; FKBP_PPIase.
Pfam, PF00254; FKBP, 1.
PR051TE; PS00453; FKBP_PPIASE 1; 1.
PR051TE; PS00454; FKBP_PPIASE 2; 1.
PROSITE; PS50059; FKBP_PPIASE 3; 1.
                                                                                                                                                                                                                                                                                                                                                     PEPTIDE BONDS IN OLIGOPEPTIDES
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NCBI_TaxID=7227;
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P48375;
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                                                                                            Wang T., Li B.Y., Danielson P.D., Shah P.C., Rockwell S.,
Wang T., Li B.Y., Danielson P.D., Shah P.C., Rockwell S.,
Echleider R.J., Martin J., Manganaro T., Donahoe P.K.;
Submitted (MAR-1996) to the EMEL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PETITE BONDS IN OLIGOPEPTIDES.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
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Mounsey A.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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1 Similarity 36.1%; Pred. No. 1.1e-07;
43; Conservative 16; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00453; FKBP PPIASE 1; 1. PROSITE; PS00454; FKBP PPIASE 2; 1. PROSITE; PS50059; FKBP PPIASE 3; 1.
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EMBL; U41441; AAA91178.1; -.
HSSP; P18203; IFKL.
FlyBase; FEGN0013954; FKE506-bp2.
InterPro; IRR01179; FKBP PPlase.
Pfam; PF00254; FKBP; 1.
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OM protein - protein search, using sw model

April 26, 2003, 06:48:54; Search time 50.5014 Seconds (without alignments) 2341.934 Million cell updates/sec Run on:

US-09-225-502-6 3054 1 MAFRGWRPPPPPLLLILLMV.....AEBFKLXDQBAKHDVTLNLA 574 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

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SUMMARIES

		Description	O8r386 musculu	Q9z247 mus musculu	095302 homo sapien	Q9yic3 gallus gall	Q9i8p8 xenopus lae	Q8vhil mus musculu	Q9h3n3 homo sapien	Q96ay3 homo gapien	O9h6n5 homo sapien	Q9h6j3 homo sapien	Q9uf89 homo sapien	Q98ud7 xenopus lae	O16309 caenorhabdi	P91180 caenorhabdi	Q95q60 caenorhabdi	Q9fjl3 arabidopsis
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dр	Query	Match Length DB	91.8	91.6	89.2	77.9	58.0	57.4	57.1	57.0	49.8	27.7	24.1	15.2	11.3	11.2	11.2	11.1
		Score	2805	2796	2723	2380.5	1772	1753.5	1744	1742	1522	845.5	736	464.5	344.5	343	343	338.5
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17 311 10.2 551 10 Q38931 18 311 10.2 551 10 Q38949 20 309 10.1 516 5 Q9V3V2 21 307 10.1 516 5 Q9V3V2 22 294.5 9.6 139 5 Q20338 24 286.5 9.6 139 5 Q20338 25 268.5 9.6 139 5 Q20338 26 268 8.8 222 4 Q9V6K3 270 8.8 222 4 Q9V6K3 28 266.5 8.8 222 4 Q9C0A4 29 266.5 8.8 222 4 Q9V6K3 26 26.5 8.8 222 4 Q9V6K3 26 26.5 8.6 151 10 Q41649 31 266.5 8.6 151 10 Q9FUL2 32 259.5 8.5 163 10 Q9FUL2 34 259.5 8.5 163 10 Q38936 35 259.5 8.9 10 Q38936 36 254.5 8.3 134 5 Q3VWB 37 255.5 8.3 134 5 Q3VWB 38 253.5 8.3 134 5 Q9V6K9 41 242.5 7.9 142 4 Q9V6K9 42 225.5 7.4 439 5 Q9VLN1 44 225.5 7.4 439 5 Q9VLN1 45 225.5 7.4 439 5 Q9VLN1	40 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Q8t109 bombyx mori Q9v178 drosophila
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ALIGNMENTS

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86 PRELIMINARY; PRT; 570 AA.	(TrEMBLrel. 21, Creat	01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	ng protein 9.	(Mouse).	Chordata;		NCBI_TaxID=10090;		SEQUENCE FROM N.A.	Taga/ -(a b) take	HILLER (AFK-2002) to the Embi/Genbank/Dubu databases. 1. RC026133: BAH26133-1: -	ICE 570 7		Query Match 91.8%; Score 2805; DB 11; Length 570;	vative 15	A RGWRPPPPPLLILLLWVTGOAAPVAGLGSDAELOIERRFVPDECPRTVRSGDFVRYHYVG		6 RGWRRRSLLLLLWYNGQAAPVLGLAVSSELQIQRSFVPDECPRIVHSGDFVRYHYVG 6.	64 TPPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERFVKIPPKLAYGNERVS 1	64 TFLDGQKFDSSYDRDSTFNVFVGKGQLIAGMDQALVGMCVNERRLVTIPPNLAYGSEGVS 1	GVI PPNSVLHFDVLLMDIMNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLF	GVIPPNSVLHFDVLLVDIWNSEDQVQIQTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLF	DSSHNRMKTYDTYVGI GWLI PGMDKGLLGMCVGEKRI I TI PPFLA YGEDGDGKDI PGQAS	DSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITVPPFLAYGEEGDGKDIPGQAS
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SEQUENCE OF 155-570 FROW N.A.

SEQUENCE-1085660; Pubmed=11217851;

WEDLINE=21085660; Pubmed=11217851;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Rasukawa T.,

Saito T., Okazaki Y., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruhl P., Batabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Bayomstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Byons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,

Nordone, P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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LVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNR 303
                   Q92247 PRELIMINARY; PRT; 570 AA.
Q92247, Q97RX5; Q9CVM0;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
FK506 binding protein 9 precursor (BC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPlase) (Rotamase) (FKBP6)
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Fkbp9 gene encoding
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                                                                     304 TFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGNIPGSAVLVFDIHVID
                                                                                                                                                                                                                                                                                                  484 YMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFT
                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss S. "Biochemical analysis of mouse FKBP60, a novel member of the FKPB family.";
                                                                                                                                                  PHNPSDSISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSG
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MEDLINE: 99453729, PubMed=10524204;
MEDLINE: A Seternes O.M., Moens U., Kraus
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Jo D., Lyu M.S., Cho B.-G., Park D., Kozak C.A., I "Identification and genetic mapping of the mouse I new member of FK506-binding protein family.";
Mol. Cells 12:272-275(2001).
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNERVS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isomerase, Rotamase, Repeat, Glycoprotein, Signal, Phosphorylation, Endoplasmic reticulum, Calcium binding.
                                                                                                                                                                                                                                                       SKELETAL
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                                                                                                                                         PROTEIN SYNTHESIS.
--- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
---- ENZYME REGULATION: INHIBITED BY FK506.
---- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
---- ILSSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, SKELETAL MUSCLE, LUNG, LIVER AND KIDNEY. LOWER LEVELS FOUND IN BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 RGWR---RRSLLLLLLLWVTGQAAPVLGLAVSSELQIQQSFVPDECPRTVHSGDFVRYHYVG
                                                                                                                                                                                                                                                                                                                       -I- PTM: PHOSPHORYLATED.
-I- STMILARLTY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS FKBP-LIKE DOMAINS.
-I- SIMILARLTY: CONTAINS 2
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DEVELOPMENTAL STAGE: EXPRESSED IN ALL DEVELOPMENTAL STAGES.
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PPIASE, FKBP-TYPE 2.
PPIASE, FKBP-TYPE 3.
PPIASE, FKBP-TYPE 4.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
PREVENT SECRETION FROM EF
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PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00453; FREF_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FREF_PPIASE_2; 3.
PROSITE; PS50059; FKBF_PPIASE_2; 3.
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Pfam; PF00254; FKBP; 4.
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Matches 524; Conservative
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                                                                  M
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                                                                    124 GVIPPNSVLHFDVLLVDIMNSEDQVHIQTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLF 183
                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                        TFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGNIPGSAVLVFDIHVID 363
                                                                                                                                  DSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLLAYGEDGDGKDIPGQAS 243
                                                                                                                                                                                                                    LVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLFDSSYSRNR 303
                                                                                                                                                                                                                                                                                                                                                                                               423
64 TFLDGQKFDSSYDRDSTFNVFVGKGQLIAGMDQALVGMCVNERRLVTIPPNLAYGSEGVS 123
                                         GVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s.;
                                                                                                                                                                                                                                                                                                                                  364 FHNPSDSISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 QVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVSGLPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99453729; PubMed=10524204;
Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Krauss E
"Biochemical analysis of mouse FKBP60, a novel member of the FKPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING PROTEIN SYNTHESIS.

CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVVLGMDMGLREMCVGEKRTVIIPPHLGYGRAGVDGBVPGSAVLVFDIEXLELVAGLPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE BONDS IN OLIGOPEPTIDES.
--- SUBCELDULAR LOCATION: INHIBITED BY FK506 (BY SIMILARITY).
--- SUBCELDULAR LOCATION: ENDOPERANIC RETICULUM (BY SIMILARITY).
--- PIM: PHOSPHORYLATED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS.
FKBP-LIKE DOMAINS.
--- SIMILARITY: CONTAINS. 2 EF-HAND CALCIUM-BINDING DOMAINS.
EMBL; BC007443; AAH07443.1; ---
                                                                                                                                                      FHNPSDSISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        095302; 0961J9; 096853; 001.MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-2002 (TrEMBLrel. 20, Last annotation update) FK506 binding protein 9 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (Prlase) (Rramase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=KIDNEY, AND MUSCLE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLAYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SIS -> HEG (IN REF. 2; AAH07443).
H -> Q (IN REF. 2; AAH11872).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GDFVRYHYVGTFPDGQKFDSSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGERRIITIPPFLAYGEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 LFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGNIPGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LFDSSYSRNRTFDTYIGGGYVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSA
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                                                                                                                                                                                                                                                                                                                                       ER (POTENTIAL)
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Pred. No. 1.1e-208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Best Local Similarity 99.0%;
Matches 510; Conservative
AAH11872.1;
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517 AA;
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432 GLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMFIWNGE 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00054; EPh; 2.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS000014; ER TARGET; UNKNOWN 1.
PROSITE; PS00054; FKEP PPIASE 2; UNKNOWN 2.
PROSITE; PS50059; FKBP PPIASE 3; 4.
SRQUENCE 564 AA; 62643 MW; 15312365BF1E43CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.0%; Score 1772; DB 13; 59.5%; Pred. No. 8.5e-133; ive 82; Mismatches 134;
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                                                                                                                                     564
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EMBL, AF233672; AAF35906.1; -.
HSSP, P2000H; IYAT.
InterPrc; IPR002048; EF-hand.
InterPrc; IPR00199; ER_target.
InterPrc; IPR00119; FKBP_Pliase.
Pfam; PF00036; efhand; 2.
Pfam; PF000254; FKBP; 4.
                          549 GDGKVTAEEFKLXDQEAK--HD
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                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         early development.";
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Best Local Similarity
Matches 329; Conserv
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHFDVLLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMK 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITSHYKPPDCSVLSKKGDYLKYHYNASLL---DGTLLDSTWNLGKTYNIVLGSGQVVLG 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
77.9%; Score 2380.5; DB 13; Length
Best Local Similarity 78.6%; Pred. No. 2.6e-181;
Matches 442; Conservative 54; Mismatches 55; Indels
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MEDLINE=98384310; PubMed=9716519;
             Q9YIC3;
01-MAY-1999 (TrEMBLrel. 10,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2002 (TrEMBLrel. 20,
CFKBP/SMAP.
PRELIMINARY;
                                                                                                                          Gallus gallus (Chicken)
                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                         CPKBP/SMAP
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SEQUENCE FROM N.A.
MEDLINE=20302564; PubMed=10842073;
Spokony R., Saint-Jeannet J.-P.;
"Xenopus FK 506-binding protein, a novel immunophilin expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 SSYDRDSTFNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKLAYGNERVSGVIPPNSVL 132
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
FK506-binding protein.

Xenopus laevis (African clawed frog).

Xenopus laevis (African Clawed frog).

Xenopus laevis (African Clawed frog).

Xenopus laevis (Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

Yenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 SITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LLLLLLLWVTGQAAPVAGLGSDAELQIERRFVPDECPRTVRSGDFVRYHYVGTFPDGQKFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 FHNPKDGITVQNQVVPQVCKRKAVTGDYVRYHYNGTLMDGALFDSSYSRNTTYNTYIGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 DIEVWHKPDSCNTTSKKGDFIKYHYNCSMLDGTLLFSSHEYETPQQVTLGSSKVIEGLDT
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01-MAR-2001
01-MAR-2001
01-JUN-2002
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424 GLLGMCVGERRTVLVPPHLAHGESGARG-VPPSAVLKFDLELLHIEEGIPDGYLFIWLQD 482
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                                               492 VSPNLFBEIDKDGNGEVLLEEFSEYIHAQVAŚGKGKLAPGFDAELIVKNMFTNQDRNGDG
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI TaxID=10090;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
65 KDa FK506-binding protein.
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                                                                                                                                                                543 KITADELKLKTEE 555
                                                                                                                                                                                                                                                                                                                                                                                        (Mouse)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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Q8VHI1
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Masuho Y., Nagahari K.;

"The human 65Apa FK506-binding protein (hFKBP65) gene induces the morphological differentiation of NT2 neuron precursor cells.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB045981; BAB20974.1; -.

REMEL; AB040881; BR-hand.

InterPro; IPR00186; ER target.

R InterPro; IPR00186; ER target.

R InterPro; IPR00186; ER target.

R Pfam; PF00154; FKBP; 4.

R Pfam; PR00154; FKBP; 4.

R PGAT; SM00054; EFP; 2.

R PROSITE; PS00014; ER TARGET: UNKNOWN 1.

R PROSITE; PS00014; ER TARGET: UNKNOWN 1.

R PROSITE; PS00044; ER TARGET: UNKNOWN 1.

R PROSITE; PS00054; FKBP PPIASE 2; UNKNOWN 1.

R PROSITE; PS00054; FKBP PPIASE 2; UNKNOWN 1.

R ROSITE; PS00054; FKBP PPIASE 2; UNKNOWN 1.

R ROSITE; PS00054; FKBP PPIASE 3; 4.

R ROSITE; PS00054; FKBP PPIASE 3; 4.

R ROSITE; PS00055; FKBP PPIASE 3; 4.
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                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 PP-----PLLLLLLWVT-----GQAAPVAGLGSDAELQIERRFVPDECPRTVRSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 FVRYHYVGTPPDGQKFDSSYDRDSTPNVFVGKGQLITGMDQALVGMCVNERRFVKIPPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNG
                                         SDSISITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVV
                                                                                                                                                                                                                                               487 IWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFDAELIVKNMFTNQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                         LGMDMGLREMCVGEKRTVI I PPHLGYGEAGVDGEVPGSAVLVFDI EXLELVAGLPEGYMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Sai
Yamamoto J., Sugano S., Isogai T.;
"HRI human cDNA sequencing project.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582
                                                                                                                                                                                                                                                                                                                                                                         547 RNGDGKVTAEEFKL---XDQEAKHD 568
                                                                                                                                                                                                                                                                                                                                                                                                            65kDa FK506-binding protein.
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Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Ota T., Nishikawa
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SEQUENCE FROM N.A.
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10 PP-----PLLLLLWVT-----GQAAPVAGLGSDAELQIERRFVPDECPRTVRSGD
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 AELIVKNMFTNQDRNGDGKVTAEEFKL---XDQEAKHD 568
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                              244 TVIPPQASLVFHVLLIDVHNPKDAVQLETLELPPGCVRRAGAGDFMRYHYNGSLMDGTLF 303
                                                                                                                                                    DSSYSRNRIFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAV 354
                                                                                                                                                                       LVFDIHVIDFHNPSDSISITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLG 413
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       176 TFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDG
                                                                                                                                                                                                                                                                                                                                                                      474 LELVAGLPEGYMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFD
                                                                                                                                                                                                                                                                                                                                                                                             SREDGLPTGYLFVWHKDPPANLFEDMDLNKDGEVPPEFFSTFIKAQVSEGKGRLMPGQD
                                                                             236 KDIPGQASLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLTYHYNGTLLDGTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rulten S., Kinloch R.A., Robinson C., Gettins L., Kay J.E.;
The Human FK506-Binding Protein Repertoire.";
L Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016467. AAH1647.1;
R EMBL; AF337909; AAH1647.1;
R InterPro; IPR001049; EF-hand.
R InterPro; IPR001179; FKBP PFIASE.
R Pfam; PF00254; FKBP PFIASE.
R Pfam; PF00254; FKBP PFIASE.
R Pfam; PF00254; FKBP PFIASE.
R PROSITE; PS00018; EF HAND; UNKNOWN 1.
R PROSITE; PS00019; EF TARGET; UNKNOWN 1.
R PROSITE; PS00019; FKBP PPIASE 2; UNKNOWN 1.
R PROSITE; PS00019; IRBP PPIASE 2; UNKNOWN 1.
R PROSITE; PS00019; FKBP PPIASE 2; UNKNOWN 1.
R PROSITE; PS00019; IRBP PPIASE 2; UNKNOWN 1.
R PROSITE; PS00019; I
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 64.2 kDa protein (65 kDa FK506-binding protein)
(EC 5.2.1.8).
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56.4%; Pred. No. 2.2e-130;
ive 99; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEKTIGDMFQNQDRNQDGKITVDELKLKSDEDEERVHE 580
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Matches 326; Conservative
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Submitted (OCT-2001)
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RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Rawabata A., Hikiji T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Ramakamura Y., Isogai T., Sugano S.; Ribi Aranka T., Nakamura Y., Isogai T., Sugano S.; Sindi A., Subaltted (AUG-2000) to the EmBL/GenBank/DDBJ databases.

RE Submitted (AUG-2000) to the EmBL/GenBank/DDBJ databases.

BRBL; ARO2569; BAB15220.1; -.

BRBL; ARO2569; IPBR.

InterPro; IPR001049; ER-hand.

BR InterPro; IPR001049; ER-hand; 2.

BR Pfam; PR0036; efhand; 2.

BR PROSITE; PS00014; ER HAND; UNKNOWN 1.

BR PROSITE; PS00014; ER PARGET; UNKNOWN 1.

BR PROSITE; PS00099; FKBP PPLASE 2; UNKNOWN 1.

BR PROSITE; PS00099; FKBP PPLASE 2; UNKNOWN 1.

BR PROSITE; PS00099; FKBP PPLASE 2; UNKNOWN 1.

BR PROSITE; PS00099; FKBP PPLASE 2; UNKNOWN 1.

BR PROSITE; PS00099; FKBP PPLASE 2; UNKNOWN 1.

BR PROSITE; PS00099; FKBP PPLASE 2; UNKNOWN 1.
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                                                                               115
                                                                                                     116 AYGNERVSGVIPPNSVLHFDVLLMDIWNSEDQVQIHTYFKPPSCPRTIQVSDFVRYHYNG 175
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                      63
6 PPSHSLIRLPLLQLLLLVVQAVGRGLGRASPAGGPLED--VVIERYHIPRACPREVQMGD
                                                                                                                                                                                                                                                                                             TFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDG
                                                                                                                                                                                                                                                                                                                       244 TVIPPQASLVFHVLLIDVHNPKDAVQLETLELPPGCVRRAGAGDFMRYHYNGSLMDGTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 LELVAGLPEGYMFIWNGEVSPNLFERIDKDGNGEVLLEEFSEYIHAQVASGKGKLAPGFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXIVVPPHLGYGEEGRGN-IPGSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 KTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVFDIHVIDFHNPSDSISITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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372 SITSHYKPPD-CSVLSKKGDYLKYHYNASILDGTLLDSTWNLGKTYNIVLGSGQVVLGMD 430
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281 LTYHYNGTLLDGTLFDSSYSRNRTFDTYIGOGYVIPGMDEGLLGVCIGEKRXIVVPPHLG 340
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                                                                                                                                                 61 YGENGTDSIGFLQGSAPLRPFRSGEGQPSLGREGGYGKTEPAYPQDPAVLGASVSSPVKW
                                                                                                                                                                                                       -----IPGSAVLVFDIHVIDFHNPSDSISITSHYKPPD-CSVLSKKGDYLKYHYN
                                                                                                                                                                                                                                                                                                          398 ASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGV
                                                                                                                                                                                                                                                                                                                                                                                                              DGEVPGSAVLVFDIEXLELVAGLPEGYMFIWNGEVSPNLFEEIDKDGNGEVLLEEFSEYI
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 KAQVSEGKGRLMPGQDPEKTIGDMFQNQDRNQDGKITVDELKLKSDEDEERVHE 353
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TISSUE-UTERUS;
Otterwaelder B., Obermaier B., Mewes H.W., Gassenhuber J.,
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, All33116; CAB61418.1;
HSSP; Q00688; 1PBK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 28.9 kDa protein (Fragment).
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InterProj IPR001896; ER target.
InterProj IPR001179; FRBP PPIase.
Pfam; PF00254; FKBP; 2.
SWART; SW00054; EFB; 2.
SWART; SW00054; EFB; 2.
PROSITE; PS00014; EF TARGET; UNKNOWN 1.
PROSITE; PS00014; EF TARGET; UNKNOWN 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
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                                                                                                         YGEEGRGN----
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                                                                                                                                                                                                            FKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPGMDKGLLGM 213
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                                                                                                                                      512 FFSEYIHAQVASGKGKLAPGFDAELIVKNMFTNQDRNGDGKVTAEEFKL----XDQEAKHD
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                                                                                                                                                                                                                                                                                                                                                                                                                 274 ISQSGDFLTYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRXI
                                                                                                                                                                                                                                                                                                                                                                                                                                            452 YGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMFIWNGEVSPNLFEBIDKDGNGEVLLE
                                                                                                      MDQALVGMCVNERRFVKI PPKLAYGNERVSGVI PPNSVLHFDVLLMDIWNSEDQVQIHTY
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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     Length 481;
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  ; Score 1522; DB 4; Length 4; Pred. No. 5.8e-113; 89; Mismatches 109; Indels
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Submitted (ANG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ARODSSH7; BAB15266.1; -.
HSSP; Q00688; 1PBK.
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InterPro; IPR002048; EF-hand.
InterPro; IPR001179; FKBP_PPIASE.
Pfam; PF000354; FKBP, 2.
SMART; SM00054; FKBP, 2.
SMART; SM00054; EFP, 2.
PROSITE; PS00014; EF TARGET; UNKNOWN 1.
PROSITE; PS500019; FK TARGET; UNKNOWN 1.
PROSITE; PS500059; FKBP_PPIASE 3; 2.
SEQUENCE 355 AA; 38950 MW; DBECF48618BF54F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA: FL72221 fis, clone HRC01651.
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45.5%; Pred. No. 3.3e-59;
iive 58; Mismatches 68;
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     Query Match
Best Local Similarity 57.5%;
Matches 276; Conservative 85
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Best Local Similarity 45.55
Matches 161; Conservative
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Q9H6J3
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                  146 DQVQIHTYFKPPSCPRTIQVSDFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIPG 205
121 TGLQGMCVGERRQLIVPPHLAHGESGARG-VPGSAVLLFEVELVSREDGLPTGYLFVWHK 179
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amano T., Yoshizato K.;
"Isolation of genes involved in intestinal remodeling during anuran metamorphosis.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP170336; AAX11511.1; -...
HSSP; 000688; 1PRW.
HSSP; 000688; 1PRW.
PFO0254; PKBP, PPIASE.
PROSITE; PS00054; PKBP, PPIASE 2; UNKNOWN_1.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKSO6-binding protein (Fragment).
Schopus laevis (African Clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                     491 EVSPNIFEEIDKDGNGEVILLEEFSRYIHAQVASGKGKLAPGFDAELIVKNMFTNQDRNGD
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1. Similarity 65.0%; Pred. No. 1.9e-29;
89; Conservative 15; Mismatches 32; Indels
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01-JAN-1998 (TrEWBLrel. 05, Last sequence update)
01-DBC-2001 (TrEWBLrel. 19, Last annotation update)
Hypothetical 29.1 kDa protein.
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                                                                                                                                                                                                                                                                                                            240 GKITVDELKLKSDEDEERVHE 260
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NCBL_TaxID=8355;
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STRAIN-BRISTOL N2;
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Rhabditidae, Peloderinae, Caenorhabditis.
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"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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"Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO16430; AAB65370.1; -.
                                                                                                                                                                 STRAIN=BRISTOL N2;
Sammons L., Wohldmann P.;
"The sequence of C. elegans cosmid CO5C8.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. - SEQUENCE 261 AA; 29080 MW; 545A8B82B1BE26AD CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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PROSITE; PS00454; FKBP PPIASE 2; UNKNOWN 1.
PROSITE; PS50059; FKBP PPIASE 3; 2.
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Interpro, IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 2.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                   24 WKDEDGLEIKIIRPIKAEKCPIKSQDGDVLDQWYKLSDKDGKEIGSNFNK-KPYTFTLGK 82
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                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                    Match 11.2%; Score 343; DB 5; Length 264; Local Similarity 37.5%; Pred. No. 2.5e-19; es 87; Conservative 36; Mismatches 93; Indels 1
                                                                                 Waterston R.;

"Direct Submission.";

Submitted (UN-2001) ro the EMBL/GenBank/DDBJ databases.

Submitted (UN-2001) 19.1;

HSSP; P20071; 1BL4.

InterPro; IPR001986; ER target.

InterPro; IPR001986; ER target.

InterPro; IPR001986; ER TARGET; UNKNOWN 1.

PROSITE; PS00014; ER TARGET; UNKNOWN 2.

PROSITE; PS00054; FKBP PPIASE 2; UNKNOWN 2.

RPROSITE; PS00059; FKBP PPIASE 3; 2.

HYPOtherical procein.

SEQUENCE 264 AA; 29937 WW; 90B79FD4FF978AZD CRC64;
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STRAIN=BRISTOL N2;
Du Z., Le T.T.;
"The sequence of C. elegans cosmid C50F2.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
   Du Z., Le T.T.;
"The sequence of C. elegans cosmid C50F2.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        095060;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 34.2 kDa protein.
C50P2.6.
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STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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"Direct Submission.";
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Amino acid sequenc	Human membrane or	Amino acid sequenc	Human pancreatic c	Hydrophobic domain	Human isomerase ho	Amino acid sequenc	Amino acid sequenc	Novel human diagno	Human polypeptide
SUMMARIES	aı	AAY23887	AAB88320	AAY23886	AAB54356	AAB12128	AAY52294	AAG79226	AAY23885	ABG05911	AA005027
	80	20	22	20	21	21	21	22	20	22	22
	Query e Match Length DB	388	570	541	434	582	582	582	441	1241	127
de	Query Match	100.0	76.7	76.3						36.6	
	Score	2106	1616	1606	1000.5	1000.5	1000.5	1000.5	997.5	771.5	618
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Himan nengtate can	2000	acta sedaen		Drosophila melanog	Drosophila melanog	Arabidopsis thalia	thali	s thali	œ	œ			Arabidopsis thalia	Λ.	Human FKBP-13 immu	Bovine mammary tis	S cerevisiae apopt	hRFKBP. Homo sapi		Polypeptide fragme			PR0381	secrete	Human PRO381 polyp	PR0381	PR0381	Human colon cancer				Human secreted pro	PR01	Bec	Human PRO1304 (UNQ	
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	7.07	25.7	23.0	13.6	13.1	12.6	12.6	12.3	12.3	12.3	12.0	12.0	12.0	11.9	11.8	11.5	11.3	11.2	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1								10.7		
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ALIGNMENTS

Human; FK506 binding protein; FKBP65; immune system disorder; immune cell; hematopoietic cell disorder; thrombolytic activity; blood coagulation disorder; blood platelet disorder; wound; heart attack; stroke; scarring; autoimmune disorder; allergic reaction; asthma; allergic asthma; respiratory problem; anaphylaxis; hypersensitivity; blood group incompatibility; organ rejection; graft versus host disease; inflammatory condition; ischemia-reperfusion injury; endotoxin lethality; arthritis; complement-mediated hyperscute rejection; nephritis; lung injury; inflammatory bowel disease; Crohn's disease; infection. Amino acid sequence of a FK506 binding protein 65. AAY23887 standard; Protein; 388 AA. (HUMA-) HUMAN GENOME SCI INC. 98US-0070875. 99WO-US00120. (first entry) 16-JAN-1999; 09-JAN-1998; 21-SEP-1999 Homo sapiens WO9935160-A1 15-JUL-1999. AAY23887; AAY23887 a

us-09-225-502-8.rag

(first entry)

23-MAY-2001

AAB88320;

Wei Y; Moore PA, Ruben SM,

WPI; 1999-430382/36.

N-PSDB; AAX86148

New nucleic acids encoding human PK506 binding proteins

Claim 12; Fig 4; 87pp; English.

The presure represents a mandam rave binning browner to the sequence given in AAX8614.

The polypeptide or polymuclectide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune calls. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells including the pluripotent stem calls to hematopoietic cells including the pluripotent stem calls in the pluripotent stem calls, in an effort to treat those disorders associated with a decrease in certain types of hematopoeitic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood coagulation disorders, blood platelet disorders or wounds resulting from trauma, surgery or other causes, or a decrease can treat heart attacks, strokes or scarring. They can also treat autoimmune disorders, allergic rections and conditions such as aethem (particularly allergic asthma) or other respiratory probleme, anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility, organ rejection or careft versus host disease, inflammatory conditions, both chronic and acute, including inflammation associated with infection, ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, near viral, bacterial, fungal and conditions, inflammatory bowel disease, or cohon's disease. present sequence represents a human FK506 binding protein 65 parasitic infections.

388 AA; Seguence

ö NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120 180 240 240 EMCVGEKRIVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEVSP 300 300 NLFEEINKVTFFCCPFVSWRRWYPEGRGQLPQDSNDSPPADLIPASWNNHMATFYPLFPN 360 NLFBEINKVTFFCCPFVSWRRWYPEGRGQLPQDSNDSPPADLIPASWNNHMATFYPLFPN 360 61 NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120 0; Gaps TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 60 9 1 TYGEIGWLIPGWDKGLLGMCVGERRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH SHYKPPDCSVLSKKGDYLXYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFHNPSDSISIT SHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR 100.0%; Score 2106; DB 20; Length 388; 100.0%; Pred. No. 9.7e-203; ive 0; Mismatches 0; Indels 0; GGGTYPEVVNDFPLKLLYFTNLNYFVLM 388 361 GGGTYPEVVNDFPLKLLYFTNLNYFVLM 388 Query Match
Best Local Similarity 100.0
Matches 388; Conservative Н 61 241 241 301 361 181 181 301 d 8 ઠ à g Ś g ò 셤 ò g ò

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121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFHNPSDSISIT 180

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AAB88320 standard; Protein; 570 AA.

RESULT, 2
AAB88320
ID AAB8
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which encode human secretory or membrane proteins represented by AABB817 - AABB8419. Included in the invention are primers
AABB817 - AABB8419. Included in the invention are primers
AABB817 - AABB8419. Included in the invention are primers
CC CDMA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polymucleotide sequences
CC can be used in vaccines. The polymucleotide sequences
CC can be used in vaccines. The polymucleotide sequences
CC can be used as sesociated with inappropriate secretory
CC diagnosis of diseases associated with inappropriate secretory
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
Sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (FCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC sa antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC agents to down regulate expression and activity. The antibodies may also
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC agents and diabetes.
CC atthritis and diabetes.
CC atthritis and diabetes. Nucleic acids encoding secretory proteins/membrane proteins, useful in 61 NPKDSISIENKVVPENCERISOSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120 Gaps 1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 60 This invention relates to nucleic acid sequences AAF93744 - AAF93916 Human, secretory protein, membrane protein, vaccine, gene therapy, rheumatoid arthritis, diabetes. Kawai Y, Sugiyama T, Hayashi K; gene therapy or as candidate target molecules in drug development ó, DB 22; Length 570; Score 1616; DB 22; Length 5 Pred. No. 3e-153; 1; Mismatches 3; Indels Human membrane or secretory protein clone PSEC0007. Claim 1; SEQ ID 8; 609pp + CD ROM; English Ota I, Isogai I, Nishikawa I, 76.7%; 98.7%; 08-JUL-1999; 99JP-0194179. 11-JAN-2000; 2000JP-0118775. 02-MAY-2000; 2000JP-0183766. 07-JUL-2000; 2000EP-0114090. Best Local Similarity 98.7 Matches 304; Conservative (HELI-) HELIX RES INST. WPI; 2001-093989/11. 570 AA; N-PSDB; AAF93747 BP1067182-A2 10-JAN-2001 Sequence Query Match 셤 ò 유 ð

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The present sequence represents human FKS06 binding protein 65 (FKBP65).

The polypeptide or polynucleotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells, to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain types of hematopoietic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood coagulation disorders, blood platelet disorders or wounds resulting from trauma, surgery or other causes, or a decrease can treat hatcks, trauma, surgery or other causes, or a decrease can treat latedck, strokes or scarring. They can also treat autoinmune disorders, allergic setting reactions and conditions such as asthma (particularly allergic asthma) or cher respiratory problems, anaphylaxis, hypersensitivity to an antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, FK506 binding protein, FKBP65; immune system disorder; immune cell; hematopoietic cell disorder; thrombolytic activity; blood coagulation disorder; blood platelet disorder; wound; heart attack; stroke; scarring; autoimmune disorder; allergic reaction; asthma; allergic asthma; respiratory problem; anaphylaxis; hypersensitivity; blood group incompatibility; organ rejection; graft versus host disease; inflammatory condition; ischemia-reperfusion injury; endotoxin lechality; arthritis; complement-mediated hyperscute rejection; nephritis; lung injury; inflammatory bowel disease; Crohn's disease; infection.
                                                                                                                                                            SHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR 434
                                                                                                                                           EMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEVSP 300
115 IPGMDEGLLGVCIGEKRIVVPPHLGYGEGRGNIPGSAVLVFDIHVIDFHNPSDSISIT
                                                              SHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding human FK506 binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a FK506 binding protein.
                                                                                                                                                                                                                                                                                                                                                                AAY23886 standard; Protein; 541 AA.
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495 NLFERIDK 502
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molecule, or blood group incompatibility, organ rejection or graft versus host disease, inflammatory conditions, both chronic and acute, including inflammation associated with infection, ischemia-reperfusion injury, endotoxin lethality, arthritis, complement—mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, or Crohn's disease. They can also be used to treat viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue tryping; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
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                                                                                                                                                            Length 541;
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                                                                                                                                                         Score 1606; DB 20;
Pred. No. 2.8e-152;
1; Mismatches 5;
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                                                                                                                                                            76.3%;
98.1%;
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N-PSDB; AAC99121.
                                                                                                                                                                             Local Similarity
                                                                                                                              541 AA;
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proteins, called parcreatic cancer antigens, given in AABS4008 to
AABS4466. The human pancreatic cancer antigens have cytostatic,
neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
gynaecological, cardiant and antiinflammatory activities, and can be used
in gene therapy. The polynucleotide and proteins can be used for
preventing, treating, or ameliorating a medical condition or in assays
for diagnosing a pathological condition or a susceptibility to one in a
subject. Binding partners to the proteins and the activity of the
cytoteins can be identified. The pancreatic cancer antigens can be used to
detect, treat or prevent pancreatic disorders, especially cancer.
Agonists and antagonists to the antigens can be used to design nucleic
analysis, tissue identification and/or typing and a variety of forensic
and diagnostic methods. The proteins can be used to design nucleic
cand diagnostic methods. The proteins can be used to generate antibodies
which are used to puxify, detect and traget the polypeptides, including
both in vivo and in vitro diagnostic and therapeutic methods. The
reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
proteins can be used to treat or prevent neural, immune system, muscular,
reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
proteins can be used to treat or prevent neural, immune system, muscular,
reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
proteins can be used to treat or prevent neural, immune system, muscular,
reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
proteins and in the exemplification of the present invention. treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition New nucleic acid that is a pancreatic cancer antigen for preventing AAC98773 to AAC99231 encode the human pancreatic cancer associated Claim 11; Page 1260-1261; 1379pp; English.

434 AA; Sequence

9 21; Gaps Query Match 47.5%; Score 1000.5; DB 21; Length 434; Best Local Similarity 55.1%; Pred. No. 1.4e-91; Matches 189; Conservative 60; Mismatches 73; Indels 21;

- 55 TYVGSGWLIKGWDQGLLGMCPGERRKIIIPPPLAYGEKGYGTVIPPQASLVFHVLLIDVH 114 9 1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH g
 - NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120 174 61 ð g
- 179 234 121 JPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI ò
- g
- LREMCYGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298 239 ò

235

g

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180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG

- g
- 354 PANLFEDMDLNXDGEVPPEEFSTFI-----KAQVSEGKGRL 389 299 SPNLFE--EINK------VTFFCCPFVSWRRWYPEGRGQL 330 ઠે 셤
- RESULT 5 AAB12128

AAB12128 standard; Protein; 582 AA.

AAB12128;

(first entry) 02-FEB-2001

Human, secreted protein, membrane protein, hydrophobic domain, proliferation control, differentiation induction, material transport, Mydrophobic domain protein from clone HP02991 isolated from KB cells. ZZXZZZZZZ ZZZZZZZZ

biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant, haematopoiesis regulator, chemotactic, chemokinetic, haemostatic, thrombolytic, anti-inflammatory, tumour inhibition, autoimmune disease, Alzheimer's disease, Parkinson's disease, cancer.

Homo sapiens

WO200029448-A2

25-MAY-2000

99WO-JP06412 17-NOV-1999; 98JP-0326255. 98JP-0364315. 99JP-0069811. 17-NOV-1998;

99JP-0138169 99JP-0119299 19-MAY-1999; 22-DEC-1998; 16-MAR-1999; 27-APR-1999;

(SAGA) SAGAMI CHEM RES CENT (PROT-) PROTEGENE INC.

Kimura T; Kato S,

N-PSDB; AAA62001, AAA62011. 2000-387753/33

membrane Proteins comprising hydrophobic regions, such as secretory and me proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -

Claim 1; Page 230-232; 410pp; English.

Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoisals activity, tissue growth activity, and throubly cactivity, and throubly cactivity, and throubly cactivity, and tinflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer.

582 AA; Seguence

238 294

21; Gaps DB 21; Length 582; 47.5%; Score 1000.5; DB 21; Length 55.1%; Pred. No. 2.2e-91; Live 60; Mismatches 73; Indels Matches 189; Conservative Local Similarity Query Match

9

9 203 TYVGSGWLIKGMDQGLLGMCPGERRKIIIPPFLAYGEKGYGTVIPPQASLVFHVLLIDVH 1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH ద ઠે

121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI 179 셤

ò 셤

180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG q ò

442

239 LREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV

ð 셤

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Human isomerase homologue; HIH; FKBP65; PPIase;
peptidy1-pro1yl dis/trans isomerase; FKS06; rapamycin;
signalling pathway; T-cell; cancer; leukaemia; testicular cancer;
melanoma; immune disorder; asthma; atherosclerosis; diagnosis; treatment;
prevention; detection; agonist; antagonist; expression; activity;
antibody; apoptosis; gene therapy; genetic immunisation; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Phosphorylated by cAMP/cGMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "FKBP-type peptidyl-prolyl cis/trans isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Endoplasmic reticulum targetting sequence"
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/note= "Phosphorylated by casein kinase II"
418
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579..582
299 SPNLFE--EINK------VTFFCCPFVSWRRWYPEGRGQL 330
                                            537
                            502 PANLFEDMDLNKDGEVPPEEFSTFI-----KAQVSEGKGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signature sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                       Human isomerase homologue-1 (HIH-1).
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                                                                                                                                                                    AAY52294 standard; Protein; 582
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/note=
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                                                                                                                                                                                                                                                                     09-FEB-2000
                                                                                                                                                                                                                      AAY52294;
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                                                                                                                                             AAY5229
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This sequence represents human isomerase homologue-1 (HIH-1).

Nucleotides encoding HIH-1 were first identified in an ovarian tumour nucleotides encoding HIH-1 were first identified in an ovarian tumour constitution of the cDNA ilbrary, the cDNA encoding this sequence being a consensus. HIH-1 is also expressed in other cancerous tissues, lymph nodes, inflamed colon, and synovium. HIH-1 has chemical and structural homology with colons, and synovium. HIH-1 has chemical and structural homology with colons in the endoplasmic reticulum targetting sequence and many of the perential phosphorylation sites. FKBPS (FKSO6 binding proteins) are a consensus isomerases of Prisass) which catalyse the cis to trans isomerisation of certain proline imidic bonds in proteins. FKBPS can bind the potent immunosuppressants FKSO6 and crapamycin, inhibiting PPIAses activity and thus blocking signalling pathways in T-cells. The expression pattern of HIH-1 and its homology with FKBPGS indicate that it plays a role in cancers (e.g., laethwama, catherosclerosis). HIH proteins, and the nucleotides that encode them, may be used for the diagnosis, treatment or prevention of such diseases. HIH proteins may be used to identify agonists and antagonists of expression and/or activity, and to raise antibodies The antibodies and antagonists of asportosis, and the antibodies may also be used in detection of HIH proteins and diagnosis of associated diseases. HIH nucleotides may be used in gene therapy or in the production of recombinant protein either protein and diagnosis of associated diseases. HIH nucleotides may be used in other antibodies may be used in gene therapy or in the production of recombinant protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention, diagnosis and treatment of cancers and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYGEIGWLI PGMDKGLLGMCVGEKRIITI PPFLAYGEDGDGKDI PGQASLVFDVALLDLH
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                                                                                                 563
/note= "Phosphorylated by casein kinase II"
                                                                             "II
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human isomerase homologs useful for
note= "Phosphorylated by casein kinase II"
                                      'note= "Phosphorylated by casein kinase II"
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                                                                                                                                                                                                                                                                                                                                                   Guegler KJ;
                                                                             'note= "Phosphorylated by casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.2e-91;
                                                                                                                                                                                                                                                                                                                                                 Hillman JL,
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Best Local Similarity 55.1
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                       Shah P,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-022783/02
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                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ32925
                      Modified-site
                                                          Modified-site
                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                       Corley NC,
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180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG 238

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263 NPKDAVQLETLELPPGCVRRAGAGDFMRYHYNGSLMDGTLFDSSYSRNHTYNTYIGQGYI 322

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Neurotrophic factor expression-inducing agent, applicable in developing drugs for neural diseases e.g. dementia, cerebral embolism, spinal injury and peripheral nerve diseases by screening their regulatory effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human neurotrophic factor expression-inducting agent. The polypeptide is designated PSEC56. The PSEC56 protein is used to increase nerve growth factor providing neurite outgrowth effect, which is applicable in developing drugs for neural diseases e.g. dementia, cerebral embolism, spinal injury and peripheral nerve diseases, with use of PSEC56 as the neurotrophic factor expression-inducing agent which can be applied in a system to study induction and secretion mechanism of neurotrophic factor.
383 RTLSRPSETCNETTKGGDFVRYHYNCSLLDGTQLFTSHDYGAPQEATLGANKVIEGLDTG 442
                                                       239 LREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
                                                                          Amino acid sequence of neurotrophic factor expression-inducing agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T, Hio Y;
Kishimoto T;
                                                                                                                                                                                                                                                                                                                                                                                             Human; neurotrophic factor; PSEC56; nerve growth factor; neurite outgrowth; neural disease; dementia; cerebral embolism; spinal injury; peripheral nerve disease.
                                                                                                                            299 SPNLFE--EINK------VTFFCCPFVSWRRWYPEGRGQL 330
                                                                                                                                                              502 PANLFEDMDLNKDGEVPPEFFSTFI-----KAQVSEGKGRL 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitsumori C, Morikawa N, Hayashi K, Nagahari K,
Nishikawa T, Isogai T, Kawasaki M, Hashimoto K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 34-38; 42pp; Japanese.
                                                                                                                                                                                                                                                     AAG79226 standard; Protein; 582 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-JP02768.
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                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                      RESULT 7
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(FREBES). It is a split the action of the sequence given in ARR86145. The polypeptide or polynucleotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells, to increase differentiation and proliferation of hematopoietic cells including the pluripotent stem cells in an effort to treat those disorders associated with a decrease in certain types of hematopoeitic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood coagulation disorders, blood platelet disorders or wounds resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; FK506 binding protein; FKBP65; immune system disorder; immune cell; hematopoietic cell disorder; thrombolytic activity; blood coagulation disorder; blood platelet disorder; wound; heart attack; stroke; scarring; autoimmune disorder; allergic reaction; asthma; respiratory problem; anaphylaxis; hypersensitivity; blood group incompatibility; organ rejection; graft versus host disease; inflammatory condition; inschmana-reperfusion injury; endocoxin lethality; arthritis; complement-mediated hyperacute rejection; nephritis; lung injury; inflammatory bowel disease; Crohn's disease; infection.
                                                                             180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG 238
                                                                                                     383 RILSRPSETCNETTKLGDFVRYHYNCSLLDGTQLFTSHDYGAPQEATLGANKVIEGLDTG 442
                                                                                                                                                            LREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
                                                                                                                                                                                121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human FK506 binding protein 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding human FK506 binding proteins
                                                                                                                                                                                                                                          299 SPNLFE--EINK------VTFFCCPFVSWRRWYPEGRGQL 330
                                                                                                                                                                                                                                                                                   502 PANLFEDMDLNKDGEVPPEEFSTFI-----KAQVSEGKGRL 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a FK506 binding protein 65.
                                                                                                                                                                                                                                                                                                                                                                                      AAY23885 standard; Protein; 441 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US00120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0070875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-430382/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY23885;
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21, Gaps

47.5%; Score 1000.5; DB 22; Length 582; 55.1%; Pred. No. 2.2e-91; ive 60; Mismatches 73; Indels 21;

Best Local Similarity 55.18 Matches 189; Conservative

Query Match

g 8

1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 60

NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGGGYV 120

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trauma, surgery or other causes, or a decrease can treat heart attacks, strokes or scarring. They can also treat autoimmune disorders, allergic reactions and conditions such as asthma asthma disorders, allergic or other respiratory problems, anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility, organ rejection or graft versus host disease, inflammation exponditions, both chronic and scute, including inflammation associated with infection, both chronic and ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperscute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, or Crohn's disease. They can also be used to treat viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                                                                                                                                                                                    242 RILSRPSETCNETIKLGDFVRYHYNCSLLDGTQLFTSHDYGAPQEATLGANKVIBGLDTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 LREMCYGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
                                                                                                                                                                                                                                                                                                                                               62 TYVGSGWLIKGMDQGLLGMCPGERRKIIIPPFLAYGEKGYGTVIPPQASLVFHVLLIDVH 121
                                                                                                                                                                                                                                                                                                                                                                                                  61 NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG
                                                                                                                                                                                                                                                                                                                               1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                         47.4%; Score 997.5; DB 20; Length 441; 55.1%; Pred. No. 2.9e-91; ive 59; Mismatches 74; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 SPNLFEEI--NK-----VTFFCCPFVSWRRWYPEGRGQL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 PANLFEDIDLNXDGEVPPEEFSTFI-----KAQVSEGKGRL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #5902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG05911 standard; Protein; 1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                Matches 189; Conservative
                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                             parasitic infections
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                                                                                                                                                                                                                              441 AA;
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                                                                                                                                                                                                                                 Sequence
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WPI; 2001-639362/73

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polypeptide (II) sequences (II) is useful as hybridisation probes, polypeptide (II) reacuted for primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome can demempain, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful in gene therapy techniques corrector normal activity of (II) or to treat disease states involving (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical and polymeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human call agreemence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cut fire, wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GCILHEGIQPRTQGTVIPPQASLVFHVLLIDVHNPKDAVQLBTLELPPGCVRRAGAGDFM 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 ------IPGQASLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFL
                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.6%; Score 771.5; DB 22; Length 1241; Best Local Similarity 49.2%; Pred. No. 7.1e-68; Matches 146; Conservative 48; Mismatches 62; Indels 41;
                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 WLI-PGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKD-----
                                                                                                                                            Claim 20; SEQ ID No 36270; 103pp; English.
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N-PSDB; AAS70098
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AAO05027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 PGMDEGLLGVCIGEKRRIVVPPHLGYGEEG-RGNIPGSAVLVFDIHVIDFHNPSDSISIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PK506 binding protein; PKBP65; immune system disorder; immune cell; hematopoietic cell disorder; thrombolytic activity; blood coagulation disorder; blood platelet disorder; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 25.9%; Score 544.5; DB 21; Length 366; Local Similarity 48.5%; Pred. No. 7.2e-46; nes 98; Conservative 37; Mismatches 66; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 2162-2164; 2338pp; English.
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                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                        08-MAR-2000; 2000WO-US05988.
                                                                                                                                                                                                           99US-0124270.
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                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
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WO200055174-A1.
                                                                                                                                                                                                           12-MAR-1999;
                                                                      21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, acg. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity is unapposed activininhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 SVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 TVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEVSPNLFEEINK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVIIPPHLGYGEAGVDGEVPGSAVLMFDIELLELVAGLPEGYMFIWNGEVSPNLFEEIDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate cancer antigen protein sequence SEQ ID NO:1692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 18919; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.3%; Score 618; DB 22; Length 1: Best Local Similarity 97.5%; Pred. No. 6e-54; Matches 117; Conservative 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Drmanac RT;
                                                                                                                                                                                                       26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                  WO200164835-A2.
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Homo sapiens.
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RESULT 11 AAB57114

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allergic reaction; asthma; allergic asthma; respiratory problem; anaphylaxis; hypersensitivity; blood group incompatibility; organ rejection; graft versus host disease; inflammatory condition; ischemia-reperfusion injury; endotoxin lethality; arthritis; complement-mediated hyperacute rejection; nephritis; lung injury; inflammatory bowel disease; Crohn's disease; infection. New nucleic acids encoding human FK506 binding proteins scarring; autoimmune Claim 12; Fig 1; 87pp; English (HUMA-) HUMAN GENOME SCI INC. 99WO-US00120. 98US-0070875. Ruben SM, WPI; 1999-430382/36. N-PSDB; AAX86145. 09-JAN-1998; Ното варіепв. 06-JAN-1999; WO9935160-A1 15-JUL-1999 Moore PA,

The present sequence represents human FKSO6 binding protein 65 (FKBP65).

The polypeptide or polymucleotide may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. They may be useful in treating or detecting deficiencies or disorders of hematopoietic cells, to increase differentiation and proliferation of hematopoietic cells, increase differentiation and proliferation of hematopoietic cells including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease con creation types of hematopoietic cells. They can be used to modulate hemostatic or thrombolytic activity, e.g. an increase can treat blood coagulation disorders, blood platelet disorders or wounds resulting from trauma, surgery or other causes, or a decrease can treat heart attacks, strokes or scarring. They can also treat autoimmune disorders, allergic reactions and conditions such as asthma (particularly allergic asthma) or other respiratory problems, anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility, organ rejection or graft versus conference, or blood group incompatibility, organ rejection or graft versus conference inflammation associated with infection, ischemia-reperfusion injury, inflammatory conditions, both chronic and acute, including inflammatics, cytokine or chemokine induced lung injury, inflammatory bowel disease, or Crohn's disease. They can also be used to treat viral, type compaterial, fungal and parasitic infections.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases

Claim 11; SEQ ID No 2257; 2922pp; English.

12 PGMDEGLLGVCIGEKRRIVVPPHLGYGEEG-RGNIPGSAVLVFDIHVIDFHNPSDSISIT 180 TGMDRGLMGMCVNERRRLIVPPHLGYGSIGLAGLIPPDATLYFDVVLLDVWNKEDTVQVS 159 181 SHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR 240 160 TLLRPPHCPRWVQDGDFVRYHYNGTLLDGTSFDTSYSKGGTYDTYVGSGWLIKGMDQGLL 219 PKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVI 121 1; Gaps 25.7%; Score 541.5; DB 20; Length 316; 48.0%; Pred. No. 1.2e-45; ive 38; Mismatches 66; Indels 1; EMCVGEKRIVIIPPHLGYGEAG 262 220 GMCPGQRRKIIIPPFLAYGEKG 241 97; Conservative Local Similarity Query Match 62 40 100 Matches ò 요 셤 셤 ò ઠે

syndrome; ovarian cancer, breast cancer; reproductive system disorder; infertility, pregnancy disorder; anovulation; polycystic ovary syndron PCOS; ovarian cysti dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive. ovarian; breast; cancer; tumour; SEQ ID NO:2257. ABP41125 standard; Protein; 166 AA. Human ovarian antigen HOFMO23, ovarian antigen; ovary; HUMA-) HUMAN GENOME SCI INC. 07-JUN-2000; 2000US-209467P. 07-JUN-2001; 2001WO-US18569 (first entry) Birse CE, Rosen CA; WPI; 2002-147878/19. N-PSDB; ABQ54202 WO200200677-A1. Homo sapiens. 23-AUG-2002 03-JAN-2002. ABP41125; RESULT 13 ABP41125

treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system clisorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian or oysts, and dysmenorrhoes), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies autoimmune oophoritis, systemic lupus erythematosus), congenital and acquired immunodeficiencies autoimmune oophoritis, gastemic lupus erythematosus, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may continue therapy, chromosome mapping, in the dentification of individuals and in forensic analysis, and the polymucletides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP41228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens of ovarian antigens of ovarian antigens of ovarian antigens.

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 DFVRYHYNGTFLDGTLFDSSHNRMKTYDTYVGIGWLIFGMDGKGLLGMCVGEKRITIFPFF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 DFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPPH 144
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                       25 RIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLHNPKDSISIENKVVPENCERISQSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                           4 RIVKIPPKLAYGSEGVSGVIPPDSVLHFDVLLMDIWNSEDQVQVHTYFTPPSCPRTIQVX 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                   23.0%; Score 484.5; DB 23; Length 166;
                                                                                                                                                                                                                                                                                       45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 LGYGEEGRG-NIPGSAVLVFDIHVIDFHNPSDSISITSHYKP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.9%; Pred. No. 2.3e-40;
tive 27; Mismatches 45
                                                                       at ftp.wipo.int/pub/published_pct_sequences.
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1es 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
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                                                                                                                                                   166 AA;
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Sequence 216 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                       55 LQADGKKFDSSFPRDQPPTFQLGAGQVIKGWDQGLLNMCVGEKRKLTIPPQLGYGDQGAG 114
                                          54; Indels 24; Gaps
                                                                                 47 QASLVFDVALLDLHNPKDSISIENKVV------PENCERISQSGDFLRYHYNGT 94
                                                                                                                   3 KSNLVISCLIL------VAISNSLVRAQDLKVEVISTPEVCEQKSKNGDSLIMHYTGT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                    154 N-IPGSAVLVPDIHVIDFHNPSDSISITSHYKPPDCSVLSKK--GDYLKYHYNA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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13.6%; Score 287; DB 22; Length 216; 37.4%; Pred. No. 2.4e-20; tive 31; Mismatches 54; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 35958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
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                                          65; Conservative
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                       Similarity
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Search completed: April 26, 2003, 06:53:07 Job time : 29.2202 secs q

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APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,386
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CLASSIFICATION DATA:
APPLICATION UNMER:
APPLICATION UNMER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REPERENCY POOR OF THE TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08989386 Patent No. 5989860 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 581 amino acida
TYPE: amino acid
STRANDEDNESS: single
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HMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 894162
US-08-989-386-7
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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1 TYGEIGWLIPGMDKGLLGMC.......VNDFPLKLLYFTNLNYFVLM 388
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-94-113-69
US-08-894-113-69
US-08-894-113-69
US-08-894-113-83
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US-08-336-618-13
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US-08-336-618-12
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

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                                                                                                                                                                                                               Gaps
                                                                                                                                                                 1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGXDIPGQASLVFDVALLDLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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48.5%; Score 1022; DB 2; Length 581;
55.8%; Pred. No. 3.8e-100;
tive 58; Mismatches 79; Indels 2
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Patent No. 5989860

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Graley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
INVERSE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SUSFTWARE: FastSEG for Windows Version 2.0
SUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3174 Porter Drive CITY: Palo Alto
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                          Best Local Similarity 55.89
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: sin
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US-08-989-386-1
    Query Match
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203 TYVGSGWLIKGMDQGLLGMCPGERRKIIIPPFLAYGEKGYGTVIPPQASLVFHVLLIDVH 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 LREMCYGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 60
                                                                                                                                                                                                                                                                                                                                                                                        47.5%; Score 1000.5; DB 2; Length 582; 55.1%; Pred. No. 7.5e-98; tive 60; Mismatches 73; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 SPNLFE--EINK------VTFFCCPFVSWRRWYPEGRGQL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502 PANLFEDMDLINKDGEVPPEEFSTFI-----KAQVSEGKGRL 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MASSACURBETES
COUNTY: U.S.A.
ZIP: 10.110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OOFBRAING SYSTEM: IBM PC. DOS (Version 3.30)
SOFWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
FILING DATE: January 17, 1992, ATTONEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AN FK506-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/052001
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAK: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/07822966B
Patent No. 5498597
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steven J. Burakoff
APPLICANT: Stuart L. Schreiber
TITLE OF INVENTION: FKBP-13, AN FKS06-17 TITLE OF INVENTION: IMMUNOPHILIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                  Matches 189; Conservative
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CITY: Boston
STATE: Massachusetts
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVARTUT01
CLONE: 2255114
                                                                                                                                              Local Similarity
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US-07-822-966B-6
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US-08-989-386-1
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63 KDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIP 122
                               30 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK 87
                                                                                       123 GMDEGLLGVCIGEKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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PCT-US92-03993-7
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Les
STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US92-03993-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Peattie, Debra A.
APPLICANT: Parding, Matthew W.
APPLICANT: Lityingelon, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: CDNA
TITLE OF INVENTION: CDNA
TITLE OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith and Reynolds, P.C.
STREET: TWO Militia Drive
                                                                                                                                                    7
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                                                                                                                                                    3; Gaps
                                                                                                                                                                                                                      29 KIQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPPVFSLGTGQVIK 86
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                                                                                                            DB 1; Length 141;
                                                                                                       tch 11.8%; Score 247.5; DB 1; Length 14 sl Similarity 47.7%; Pred. No. 1.5e-18; 51; Conservative 18; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                              123 GMDEGLLGVCIGEKRIVVPPHLGYGEEGR-GNIPGSAVLVPDIHVI 168
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FOC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.8%; Score 247.5; DB 1; Best Local Similarity 47.7%; Pred. No. 1.5e-18; Matches 51; Conservative 18; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLIANCE DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,75:
FILING DATE: 11-OCT-1991
PRIOR APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 07/777,752
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Patent No. 5763590
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TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,227
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      not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 142 amino acids
TYPE: amino acid
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CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-336-618-18
                        TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                            dest Local Similarity
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ZIP: 02173
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STRANDEDNESS:
                                                 ; MOLECULE TYI
US-07-822-966B-6
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                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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Sequence 20, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Harding, Matthew W.
TITLE OF INVENTION: RFKBP: A NOVEL PROLYL ISOMERASE AND TITLE OF INVENTION: RFKBP: A NOVEL PROLYL ISOMERASE AND TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Militia Drive
STREET: Two Militia Drive
CITY: Lexington
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
CLASSIFICATION NUMBER: PCT/US92/03993
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFRENCE/DOCKET NUMBER: VP191-05A PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1961-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 142 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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   PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 SLVFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLD-GTLFDSSYSR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GSPIAFELGVGRVIKGWDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPPSADLVFDVE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Score 237.5; DB 1; Length 135; 43.1%; Pred. No. 1.6e-17; tive 22; Mismatches 41; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08803899
Patent No. 531224
GENERAL INFORMATION:
APPLICANT: DONABOE, PATRICIA K.
APPLICANT: WANG, TONGWEN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING
TITLE OF INVENTION: CELLULAR RESPONSE TO TGF-BETA LIGANDS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 NEW YORK AVENUE, SUITE 600
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF FITLE OF INVENTION: CDNA NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Conservative
                                                                             STREET: Two Militia D
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-336-618-20
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                         ZIP: 02173
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128 LVD 130
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63 KDSISIENKAVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 236.5; DB 2; Length 141; 46.7%; Pred. No. 2.2e-17; trive 18; Mismatches 36; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.2%; Score 235; DB 3; Length 104; Best Local Similarity 47.9%; Pred. No. 2e-17; Matches 46; Conservative 16; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GMDEGLLGVCIGEKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 168
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Patent No. 6090612
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Medical Research Council
FITUE OF INVENTION: Adenylate cyclase and uses therefor
FILE REFERENCE: P14716C
CURRENT APPLICATION NUMBER: US/08/894,173A
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BA PC compatible
COMPUTER: BA PC compatible
COMPUTER: PATEMIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,899
FILING DATE: 02/21/1997
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/012,054
FILING DATE: 02/22/1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202)371-2600
INTELERAX: (202)371-2540
INTELERAX: (202)371-2540
INTELERAX: SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS:
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MOLECULE TYPE: protein
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Matches 50, Conserva
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-894-173-86
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LENGTH: 104
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TYPE: PRT
ORGANISM: Human
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                                                                                                                                                           US-09-398-193-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DHCPIKSRRKDDVLHMHYTGKLBDGTEFDSSLPQNQPFVFSLGTGQVIKGWDQGLLGMYBG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 DCLIKAMPGDKVKVHYTGSLESGTVFDSSYSRGSPIAFELGVGRVIKGWDQGVAGMCVGE 67
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                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 235; DB 4; Length 10 47.9%; Pred. No. 2e-17; cive 16; Mismatches 34; Indels
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TILE OF INVENTION: Adenylate cyclase and uses therefor
FILE REPERENCE: P14716C
CURRENT APPLICATION NUMBER: US/08/894,173A
CURRENT FILING DATE: 1997-08-13
SOFTWARE: PATENTING Ver. 2.1
SEQ ID NO 84
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Patent No. 6197581
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor FILE REFERENCE: P24360-
                                                                                                                                                       APPLICAT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
FILE REPERENCE: P24360-
CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 86
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 232.5; DB 3;
49.5%; Pred. No. 3.7e-17;
tive 15; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 KRKLQIPSSLAYGERGVPGVIPPSADLVFDVELVDV 103
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; Sequence 84, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
                                                                               US-09-398-193-86; Sequence 86, Application US/09398193; Patent No. 6197581; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.59
Matches 47, Conservative
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Matches 46; Conservative
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; TYPE: PRT
; ORGANISM: Human
US-08-894-173-84
                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Yeast
US-09-398-193-86
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US-09-398-193-84
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63 KDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIKGWDQGLLGMYEG 62
                                                                                                                                                                                                                                             Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application PC/TUS9203993
GENERAL INFORMATION:
APPLICANT: Harding, Matthew W.
TITLE OF INVENTION: RFKBP: A NOVEL PROLYL ISOMERASE AND
TITLE OF INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 99
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03993
FILING DATE: 19920507
                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.4%; Score 218; DB 5; 49.4%; Pred. No. 1.2e-15;
                                                                                                                                                                                                                                           11.0%; Score 232.5; DB 4
49.5%; Pred. No. 3.7e-17;
iive 15; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                        135 EKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 EKRKLVIPSELGYGERGAPPKIPGGATLVFEVELL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/697,113
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Conservative
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.55
Matches 47; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lexington
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Search completed: April 26, 2003, 06:49:53 Job time : 12.0671 secs
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                                                                                                                                                                        RESULT 13
US-00-894-173-69
iSequence 69, Application US/08894173A
iPerent No. 609612
iGENERAL INFORMATION:
APPLICANT: Medical Research Council
iTILE REFERENCE: P14716C
CURRENT APPLICATION: Medical NUBBER: US/08/894,173A
CURRENT PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 97
iSEQ ID NO 69
LENGTH: 107
iTENGTH: 107
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Parent No. 6090612
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
FILE REFERENCE: P14716C
CURRENT APPLICATION NUMBER: US/08/894,173A
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
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                                            66 GWDQGLLGMCEGEKRKLVIPSELGYGERG 94
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Patent No. 6197581
PARENAL INFORMATION:
APPLICANT: Medical Research Council
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LENGTH: 107
TYPE: PRT
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US-08-894-173-83
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79 RISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRR 138
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                                                                                                                                                                                                                                                                                                       Length 107;
                                                                                                                                                                                                                                                                                               ; Score 208.5; DB 4; Length
; Pred. No. 1.4e-14;
16; Mismatches 34; Indels
TITLE OF INVENTION: Adenylate cyclase and uses therefor
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CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 69
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.0%;
Matches 40; Conservative 10
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Neurospora crassa
US-09-398-193-69
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April 26, 2003, 06:51:02 ; Search time 12.2714 Seconds (without alignments) 2533.559 Million cell updates/sec
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1 TYGEIGWLIPGMDKGLLGMC......VNDFPLKLLYFTNLNYFVLM 388
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1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

Description	Sequence 8, Appli	Sequence 6, Appli	Sequence 808, App	Sequence 4, Appli	Sequence 1692, Ap	Sequence 2, Appli	Sequence 145, App		Sequence 145, App		Sequence 4, Appli	Sequence 145, App	Sequence 384, App	Sequence 384, App	Sequence 384, App	Sequence 384, App	Sequence 384, App	Sequence 384, App	Sequence 384, App
QI	US-09-225-502-8	US-09-225-502-6	US-09-925-297-808	US-09-225-502-4	US-09-925-300-1692	US-09-225-502-2	US-09-978-295A-145	US-09-978-697-145	US-09-978-192A-145	US-09-999-832A-145	US-10-001-054-4	US-09-978-189-145	US-10-028-072-384	US-10-121-049-384	US-10-123-904-384	US-10-140-470-384	US-10-175-746-384	US-10-176-918-384	US-10-176-921-384
DB	10	10	10	10	10	10	0	σ	σ	σ	σ	6	σ	Φ	δ	6	6	σ	δ
* Query Match Length DB	388	574	434	441	366	336	211	211	211	211	211	211	211	211	211	211	211	211	211
% Query Match	100.0	76.3	47.5	47.4	25.9	25.7	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.1
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US-10-137-865-384 US-10-140-474-384 US-10-142-431-384 US-10-143-114-384	10-140-002-304 10-978-608A-14 10-076-724A-18 10-978-191A-14 10-978-403A-14	US-09-978-585A-145 US-10-017-081A-145 US-10-123-262-384 US-10-142-423-384 US-09-978-824-145 US-09-981-915A-145 US-09-991-833A-145 US-09-10-121-050-384	
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ALIGNMENTS

RESULT 1 US-09-225-502-8 ; Sequence 8, A; ; Patent No. US	SULT 1 -09-225-502-8 Sequence 8, Application US/09225502A Patent No. US20020137127A1
GENERAL I APPLICAN TITLE OF	GENERAL INFORMATION: APPLICANT: Moore et al. TITLE OF INVENTION: Human FK506 Binding Proteins
CURRENT	FILE REFERENCE: PF392 CURRENT APPLICATION NUMBER: US/09/225,502A THE PERSON TITING DAME: 1000-01-06
PRIOR AI	CORRELL FILLING LAILS (1975) PRIOR FILLING DATE: 1998-01-09
SOFTWARE:	OF SEQ ID NOS: 8
LENGTH: 388	1.388 1.388
, ORGANISM: H US-09-225-502-8	AIREN Homo sapiens 9-225-502-8
Query Match	
Best Loca Matches	Best Local Similarity 100.0%; Fred. NO. 1.46-186; Matches 388; Conservative O; Mismatches O; Indels O; Gaps O;
Oy 1 5	TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 60
op 1,	TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGBGKDIPGQASLVFDVALLDLH 60
Qy 61]	NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGGGYV 120
Db 61]	NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGGGYV 120
Oy 121	IPGMDEGLIGUCIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFHNPSDSISIT 180
Db 121	
Qy 181	SHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR 240
181 40	SHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLR 240
Oy 241	EMCYGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEVSP 300

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PRIOR FILING DATE: 1999-03-12
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US-09-225-502-4
                                                                     LENGTH: 434
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                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFHNPSDSISIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMCVGEKRIVIIPPHLGYGEAGVDGEVPGSAVLVFDIEXLELVAGLPEGYMFIMNGEVSP 494
                                                               301 NIEEINKVIFFCCPFVSWRRWYPEGRGQLPQDSNDSPPADLIPASWNNHMATFYPLFPN 360
241 EMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMF1WNGEVSP 300
                                   301 NLFEEINKVTFFCCPFVSWRRWYPEGRGQLPQDSNDSPPADLIPASWNNHMATFYPLFPN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 TYVGIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 808, Application US/09925297
Batent No. US20020081659A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPRENCE: PALO.
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                                APPLICANT: Moore et al.
TITLE OF INVENTION: Human FK506 Binding Proteins
FILE REFERENCE: PF392
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/225,502A
CURRENT FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/070,875
PRIOR PILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                           361 GGGTYPEVVNDFPLKLLYFTNLNYFVLM 388
                                                                                                       361 GGGTYPEVVNDFPLKLLYFTNLNYFVLM 388
                                                                                                                                                                                                                           Sequence 6, Application US/09225502A Patent No. US20020137127A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-225-502-6
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US-09-225-502-6
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LENGTH: 574
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61 NPKDSISIENKVVPENCERISQSGDFLRXHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120
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Best Local Similarity 55.1%; Pred. No. 5.9e-85;
Matches 189; Conservative 59; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 47.5%; Score 1000.5; DB 10; Lengt Best Local Similarity 55.1%; Pred. No. 3e-85; Matches 189; Conservative 60; Mismatches 73; Indels
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CURRENT APPLICATION NUMBER: US/09/225,502A
CURRENT FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/070,875
PRIOR FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
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NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 808
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-225-502-4
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US-09-925-297-808
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, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1692
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180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG 238
                     242 RILSRPSETCNETIKLGDFVRYHYNCSLLDGTOLFTSHDYGAPQEATLGANKVIEGLDTG 301
                                                                         LREMCVGEKRTVI I PPHLGYGEAGVDGEVPGSAVLVFDI ELLELVAGLPEGYMFIWNGEV
                                                                                                                                                                                                                                                                                                                                GUREALL AND LATE CATAINS COREN,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR PAPLICATION NUMBER: PC7/US00/05988
PRIOR PILING DATE: 12000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 1692
LENGTH: 366
                                                                                                                                                                         361 PANLFEDIDLAKOGEVPPEEFSTFI-----KAQVSEGKGRL 396
                                                                                                                                                 299 SPNLFEEI -- NK------VTFFCCPFVSWRRWYPEGRGQL 330
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Patent No. US20020137127A1
GENERAL INFORMATION:
APPLICANT: Moore et al.
TITLE OF INVENTION: Human FK506 Binding Proteins
FILE REPERENCE: PF392
CURRENT APPLICATION NUMBER: US/09/225,502A
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PRIOR APPLICATION NUMBER: 60/070,875
                                                                                                                                                                                                                                                                                Sequence 1692, Application US/09925300 Patent No. US20020151681A1 GENERAL INFORMATION:
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FEATURE:
NAME/KEY: SITE
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US-09-925-300-1692
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US-09-225-502-2
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE RESERBENCE: PS630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
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                                                                                                                                                                                                                                                                                                       62 PKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVI 121
                                                                                                                                                                                                                                                                                                                                      40 PLEDVVIERYHIPRACPREVQMGDFVRYHYNGTFEDGKKFDSSYDRNTLVALVVGVGRLI 99
                                                                                                                                                                                                          Length 336;
                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                             .6e-42;
                                                                                                                                                                                                                                                        38; Mismatches
                                                                                                                                                                                                          25.7%; Score 541.5;
48.0%; Pred. No. 1.6
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 GMCPGQRRKIIIPPFLAYGEKG 241
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
    1998-01-09
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Gerritsen, Mary B.
Goddard, Audrey
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PRIOR FILING DATE: 1998-01-0
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 336
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Kuo, Sophia S.
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Eaton, Dan
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                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-225-502-2
                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 97; Conserv
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R FILING DATE: 1998-04-01

A APPLICATION NUMBER: 60/080333

R FILING DATE: 1998-04-01

R PILING DATE: 1998-04-01

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/081070 R FILING DATE: 1997-11.21

R APPLICATION NUMBER: 60/077450

R FILING DATE: 1998-03-10

R APPLICATION NUMBER: 60/077632

R FILING DATE: 1998-03-11

R APPLICATION NUMBER: 60/077641

R RILING DATE: 1998-03-11

R APPLICATION NUMBER: 60/077649

R FILING DATE: 1998-03-11

R PILING DATE: 1998-03-12

R PILING DATE: 1998-03-12

R PILING DATE: 1998-03-12 TLING DATE: 1998-03-27
PPLICATION NUMBER: 60/079689
TLING DATE: 1998-03-27
PPLICATION NUMBER: 60/079663
TLING DATE: 1998-03-27 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080327 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080328 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081049 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081071 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081195 FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20 PLICATION NUMBER: 60/079786 LING DATE: 1998-03-27 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081203 APPLICATION NUMBER: 60/081229 ING DATE: 1998-04-09 LICATION NUMBER: 60/081955 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 PLICATION NUMBER: 60/079656 LING DATE: 1998-03-26 APPLICATION NUMBER: 60/080165 APPLICATION NUMBER: 60/081817 APPLICATION NUMBER: 60/079728 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080194 APPLICATION NUMBER: 60/078886 APPLICATION NUMBER: 60/078939 APPLICATION NUMBER: 60/079664 LICATION NUMBER: 60/079920 APPLICATION NUMBER: 60/079923 APPLICATION NUMBER: 60/065311 TLING DATE: 1998-03-30 FILING DATE: 1998-04-09 1998-04-15 ILING DATE: 1998-03-13 ILING DATE: 1998-03-31 NG DATE: 1998-03-27 ILING DATE: 1998-03-31

PLICATION NUMBER: 60/083558 LING DATE: 1998-04-29 PLICATION NUMBER: 60/083559 FILING DATE: 1998-04-30
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FILING DATE: 1998-05-05
FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085338 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083495 ILING DATE: 1998-04-29
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R FILING DATE: 1998-03-26
A APPLICATION NUMBER: 60/079664
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A APPLICATION NUMBER: 60/079683
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RAPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/080107
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APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/077641
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
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FILING DATE: 1998-03-25
APPLICATION NUMBER: 60/079656
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APPLICATION WINBER: 60/079728
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/080165
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/081203
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
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APPLICATION WIMBER: 60/078886
ELING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/080334
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FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 211;
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PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
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Gurney, Austin L.
Hillan, Kenneth J
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Patent No. US20020169284A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Goddard, Audrey
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Filvaroff, Ellen
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity 36.84
Matches 46; Conservative
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Gao, Wei-Qiang
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R PILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/082568
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R APPLICATION NUMBER: 60/082569
R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/08204
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A APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/083392
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FILING DATE: 1998-04-23
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APPLICATION NUMBER: 60/083742
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APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/085338
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same *FILE REFERENCE: P2630P1C9

Paoni, Nicholas F. Roy, Margaret Ann Shelton, David L. Stewart, Timothy A.

Tumas, Daniel Williams, P. Mickey Wood, William I.

> APPLICANT: APPLICANT:

Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J

Kljavin, Ivar J. Kuo, Sophia S.

APPLICANT

Napier, Mary A.

Pan, James;

APPLICANT APPLICANT APPLICANT

Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey

APPLICANT

Ferrara, Napoleon Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17

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51 VFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLRYHYNGTL-LDGTLFDSSYSRNR 109
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR APPLICATION NUMBER: 60/08569
PRIOR PILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/08559
PRIOR APPLICATION NUMBER: 60/08559
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
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R APPLICATION NUMBER: 60/085700

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R APPLICATION NUMBER: 60/085579

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Patent No. US20020177553A1
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Best Local Similarity 36.84
Matches 46; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Eaton, Dan
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132 LEIRN 136
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
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APPLICANT: Tumme, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 GQPIWFTLGILEALKGWDQGLKGMCVGBKRKLIIPPALGYGKBGKGKIPPBSTLIFNIDL 131
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                                                                                                                                                                                                                                                                                      / Match 11.1%; Score 234.5; DB 9; Length 211; Local Similarity 36.8%; Pred. No. 4e-14; nes 46; Conservative 29; Mismatches 47; Indels 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 145, Application US/0999832A Publication VO US20020192706A1
BUBICAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bocstein, David
APPLICANT: Bocstein, David
           R FILING DATE: 1998-05-15

R APPLICATION NUMBER: 60/08500

R APPLICATION NUMBER: 60/085689

R APPLICATION NUMBER: 60/085689

R FILING DATE: 1998-05-15

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R APPLICATION NUMBER: 60/08550

R APPLICATION NUMBER: 60/08550
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR PLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION WUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
APPLICATION NUMBER: 60/085582
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
Fong, Sherman
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Kuo, Sophia S.
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Pan, James;
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R APPLICATION NUMBER: 60/064249
R FILING DATE: 1997-11-03
R APPLICATION NUMBER: 60/065311
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R FILING DATE: 1998-03-13
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ILING DATE: 1998-03-25
PPLICATION NUMBER: 60/079656
ILING DATE: 1998-03-26
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PPLICATION NUMBER: 60/079786
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FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/080327
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PPLICATION NUMBER: 60/080334
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Sequence 4, Application US/10001054 Publication No. US20020192209A1 GENERAL INFORMATION:

US-10-001-054-4

Baker, Kevin Goddard, Audrey Gurney, Austin Hebert, Carolyn

APPLICANT: Henzel, William
APPLICANT: Henzel, William
APPLICANT: Kabakoff, Rhona
APPLICANT: Shelton, David
APPLICANT: Shelton, David
APPLICANT: Shelton, David
APPLICANT: Shelton, David
APPLICANT: Shelton, David
APPLICANT: Wateanabe, Colin
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APPLICANT: Wateanabe, Colin
FILE REFERENCE: P3034R1PCT
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P3034R1PCT
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1 Similarity 36.8%; Pred. No. 4e-14;
46; Conservative 29; Mismatches 47;
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                                                                                                                                                                                                                                                                                           Length 211;
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PRIOR PELICATION NUMBER: 09/918585
PRIOR PELING DATE: 2001-10-15
PRIOR PLING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
              PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/USO1/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/USO1/21735
PRIOR PRILING DATE: 2001-07-09
PRIOR PLILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2010-08-29
APPLICATION NUMBER: PCT/US01/19692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 145, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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Grimaldi, J. Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Wood, William I.
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
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Goddard, Audrey
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Botstein, David
Desnoyers, Luc
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Kuo, Sophia S.
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.8*
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wei-Qiang
                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-4
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US-09-978-189-145
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R APPLICATION NUMBER: 60/081819
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R APPLICATION NUMBER: 60/082568
R FILING DATE: 1998-04-21
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R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-30
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R APPLICATION NUMBER: 60/084366
R APPLICATION NUMBER: 60/084414
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084411
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084431
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084637
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R FILING DATE: 1998-05-07
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A APPLICATION NUMBER: 60/082700
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A APPLICATION NUMBER: 60/082796
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# FILING DATE: 1998-04-27
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# FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/084627
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APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083559
'ILING DATE: 1998-04-29
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FILING DATE: 1998-05-07
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FILING DATE: 1998-05-13
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR APPLICATION NUMBER: 60/085699
PRIOR PILING DATE: 1998-05-15
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PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR PILING DATE: 1998-05-15
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PRIOR FILING DATE: 1997-08-26
PRIOR PELING DATE: 1997-08-26
PRIOR PEPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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o. US20030004311A1
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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Tumas, Daniel
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Gurney, Austin L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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PRIOR PALLONION NUMBER: 60/05363

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R APPLICATION NUMBER: 60/085697
R FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07 FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/087106 FILING DATE: 1998-05-28 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088730 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088741 TLING DATE: 1998-03-12 PPLICATION NUMBER: 60/078910 APPLICATION NUMBER: 60/088026 APPLICATION NUMBER: 60/084627 PRIOR API PRIOR API PRIOR API PRIOR API PRIOR API PRIOR API PRIOR PI OR
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                110 TFDTVIGQGYV--IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHV 167
                                                                                                         72 GQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKBGKGKIPPESTLIFNIDL 131
      51 VFDVALLDLHNPKDSISIENKVVPENCERISQSGDFLRYHYNGTL-LDGTLFDSSYSRNR 109
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                            12 LFVTSLIGALIPEPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSLFHSTHKHNN 71
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11.1%; Score 234.5; DB 9;
Best Local Similarity 36.8%; Pred. No. 4e-14;
Matches 46; Conservative 29; Mismatches 47;
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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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                                                                                                                                                                                                                                                                                                     Sequence 384, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
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Stewart, Timothy A.
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Gao, Wei-Qiang
Gerritsen, Mary E.
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R117
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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            R FILING DATE: 1998-06-23

DR APPLICATION NUMBER: 60/090429

DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090863

DR FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/091860

DR FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/091860

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 384, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/090349
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Best Local Similarity 36.8
Matches .46; Conservative
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Best Local Similarity
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US-10-121-049-384
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Length 211; Indels

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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 26, 2003, 06:48:54; Search time 12.2714 Seconds (without alignments) 3039.596 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-225-502-8
2106
1 TYGEIGWLIPGMDKGLLGMC......VNDFPLKLLYFTNLNYFVLM 388

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ription	FKBP65 binding pro	hypothetical prote	_		_	hypothetical prote	peptidylprolyl iso	protein ZC455.10 [peptidylprolyl iso	probable peptidylp	probable peptidylp	hypothetical prote	probable peptidylp	FK506-binding prot	peptidylprolyl iso	binding protein -	probable peptidylp	FK506/rapamycin-bi	peptidylprolyl iso	probable peptidyl-	FKBP-type peptidyl	FK506-binding prot	peptidyl-prolyl ci	FKBP-type peptidyl	hypothetical prote	peptidyl-prolyl ci	FK506-binding prot	peptidyl-prolyl ci	hsp 90-binding pro
	9669	607	741	9780	7586	382	5383	251	6228	060	238	538	237	748	485	999	489	365	337	180	878	060	347	144	537	431	422	331	386 🖊
	1496	T42709	T31741	T297	T27	T21882	S55	E897	8462	T12090	8712	T26538	8715	JT0748	872485	1496	T06489	301	825337	A83180	AH1878	811090	B753	87514	T2653	C824	JC542	D823	A42
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RESULT 2 T42709

peptidylprolyl iso immunophilin FKBP5 FK506-binding prot	hypothetical prote peptidyl-prolyl ci peptidylprolyl iso	hypothetical prote peptidylprolyl iso hypothetical prote	peptidyl-prolyl ci immunophilin p59 - FK506-inhibitable	peptidylprolyl iso FK506-binding prot	Pepring in 150 FKBP-type peptidyl
A33146 A46372 S54139	T21594 T40724 AE0429	T26539 A61431 A64155	F83075 JN0873 A40211	A35780 A42657 E92022	F91153
01 01 01	000	0 0 0	0 0 0	0 0 0	7 (7
114 459 108	431 112 206	108 107 241	205 458 105	108	270
8 8 8 6 6 8	8 8 6 7 9 5	8 8 8 7 4 4		8 8 9	8:1
188 188 184.5	183 182 179	178 177 176	175 175 174.5	173	171.5
30 31 32	33 34 35	36 38 38	39 4 4 10	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	45

ALIGNMENTS

RESULT 1 149669 FYRBP65 bi C, Species in C, Species in C, Accessin R, Simek, Genomics A, Title: A, Referent A, Referent A, Referent A, Referent A, Referent A, Referent A, Status: A, Status: C, Superfa P, 1094 F, 173-226 F, 173-226 F, 198-445	RESULT 1 119669 FREP66 binding FREP66 binding C.Species: Mus C.Accession: 14 R.Accession: 14 R.A.Title: Sequer A.Reference num A.Reference num A.Residues: 1- A.Residues: 1- A.Cross-refere: 1- A.Cross-refere: 1- F:61-108/Domair F:61-13-220/Domai F:285-332/Domai	protein - mouse musculus (house mouse) 1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999 19669 19669 17-409, 1993 17-409, 1993 18-18-18-18-18-18-18-18-18-18-18-18-18-1	chromosc
Out Bee Mat	Query Match Best Local Matches 19	Query Match 48.5%; Score 1022; DB 2; Length 581; Best Local Similarity 55.8%; Pred. No. 2.5e-76; Matches 198; Conservative 58; Mismatches 79; Indels 20; Gaps 6;	.:5
λ α	1 202	1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH 60 	
ò 8	61	NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120 ::: : : ::	
& g	121 322	IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI 179 :	
දි දි	180	TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG 238 : :	
දි සි	239	LREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298	
දු පු	299	SPNLEBEINKVTEFCCPFVSWRRWYPEGRGQL-PQDSNDSPPADL 342 : ::: : : :: : : STSLFEDMDINKDGEVPPEEFSSFIKAQVNEGKGRLMPGQDPDKTISDM 549	

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89 IAMEGMCVGEQRKVIIPPPEQGFDEDG-DEVEGKGETLYYFVELKSIFRPKPGAKWITDEG 147
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A;Molecule type: DNA
A;Residus: 1-261 <SAM>
A;Cross-references: EMBL:AF016430; PIDN:AAE65370.1; GSPDB:GN00023; CESP:C05C8.3
A;Cross-references: strain Bristol N2; clone C05C8
C;Genetics:
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                C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Species: Caenorhabditis elegans
C'Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 02-Sep-2000
C'Accession: T31741
R'Sammons, L.; Wohldmann, P.
submitted to the RMBL Data Library, July 1997
A'Describtion: The sequence of C. elegans cosmid C05C8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 YVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 SITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EIRTLSRPSETCNETTKLGDFVRYHYNCSLLDGTQLFTSHDYGAPQEATLGANKVIEGLD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                          C.Accession: T42709 Fortain 1. Mewes, H.W.; Gassenhuber, J.; Wiemann, Submitted to the Protein Sequence Database, November 1999
A.Reference number: Z22231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Superfamily: BKBP-type peptidylprolyl isomerase homology
F;48-94/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
F;166-213/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                          A,Note: DKFZp58610821.1
C;Superfamily: BKBP-type peptidylprolyl isomerase homology
F;79-126/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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180 DPPANLFEDMDLNKDGEVPPEEFSTFI-----KAQVSEGKGRL 217
                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL133116
A;Experimental source: adult uterus; clone DKFZp58610821
hypothetical protein DKFZp586I0821.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.2%; Score 572.5; DB 2; Best Local Similarity 48.9%; Pred. No. 1e-39; Matches 110; Conservative 45; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C05C8.3 - Caenorhabditis elegans
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-262 <AAA>
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Best Local Similarity
Matches 74; Consery
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A, Map position: 5
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T2-Oct-1999 #text_change 02-Sep-2000
C;Accession: T27586
R;Lightning, J.
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-264 < DUZ>
A; Cross-references: EMBL: U80445; PIDN: AAB37799.1; GSPDB: GN00019; CESP: C50F2.6
A; Experimental source: strain Bristol N2; clone C50F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C50F2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T29780
R;Du, Z.; Le, T.T.
Submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid C50F2.
                                                                      63 KDSISIENKVV----PENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 YVIPGMDEGLLGVCIGEKRRIVVPPHLGYGBEG--RGNIPGSAVLVFDIHVIDFH---- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 16; Gaps
177 ISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NPSDSISITSHYK-PPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1
A;Introns: 75/2, 205/3
A;Introns: 75/2, 205/2
C;Superfamily: BKBP-type peptidylprolyl isomerase homology
F;50-96/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
F;171-218/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
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                                                                                                                                                                                                                                                                                                 237 MGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.3%; Score 344; DB 2; Lv Best Local Similarity 33.9%; Pred. No. 7.5e-21; Matches 80; Conservative 45; Mismatches 95;
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protein ZC455.10 [imported] - Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: To-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
CiAccession: B89251
Rianorymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
Aithle: Genome sequence of the nematode C. elegans: a platform for investigating bi Aireference number: A75000; WUID:99059613; PMID:9851916
Ainote: see websites genome.wustl.edu/gsCC_clegans/ and www sanger.ac.uk/Projects/CAinote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                                                                                                                isomerase hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:chr_V; PIDN:CAA99959.1; PID:g3881406; GSPDB:GN00023; CESP:ZC4
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                                                                                                            A.Gene: FKBP70
C.Superfamily: peptidylprolyl isomerase ROF1; BKBP-type peptidylprolyl isom
C.Superfamily: peptidylprolyl isomerase; cyclosporin A binding
C;Keywords: calmodulin binding; cis-trans-isomerase; cyclosporin A binding
F;60-107/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
F;176-219/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
F;293-341/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
F;415-448/Domain: tetratricopeptide repeat homology <TTI>
F;484-517/Domain: tetratricopeptide repeat homology <TTI>
                                                A;Residues: 1-559 <OSH>
A;Cross-references: EMBL:X86903; NID:g854625; PIDN:CAA60505.1; PID:g854626
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 LRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPPHLG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 ISIENKWYPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 EGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFH--NP-----SDSI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 DGKDIPGQASLVFDVALLDL---HNPKDSISIENKVVPENCER-----ISQSGDF 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DDFDIPAGDDMAMGDGMGDFGGAEGPGMKVGEENEIGKQGLKKKLLKEGEGWDTPEVGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --YLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 YGEEGR-GNIPGSAVLVFDIHVIDFHNPSDSISITSHYKPPDCSVLSKKGD-----
                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 559;
                                                                                                                                                                                                                                                                                                                                                           13.5%; Score 283.5; DB 1; Length 29.5%; Pred. No. 2.1e-15; tive 43; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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30.8%; Pred. No. 4.3e-15;
ive 39; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLGYGE-----AGVDGEVPGSAVLVFDIELL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     80; Conservative
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                         A; Molecule type: mRNA
A; Residues: 1-559 <0SH>
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Best Local S
Matches 70
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Matches
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A,Introns: 43/2; 80/3
C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase
F;45-92/Domain: BKBP-type peptidylprolyl isomerase homology <PFI>
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N;Alternate names: FK506-binding protein; peptidylprolyl cis-trans isomerase; PPIase
C;Species: Triticum aestivum (common wheat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: S55383
R;Oshra, B.; Breiman, A.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S55383
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T21882
R;Kerbahaw, J.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19482
A;Accession: T21882
A;Accession: T21882
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-139 <WIL>
A;Residues: 1-139 <WIL>
A;Experimental source: Clone F36H1
C;Genetics:
                                                                                                                                                                                                                                      66 ISIBNKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMD 125
                                                                                                                                                                                                                                                                                                                                    126 EGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFH--NP-----SDSI 177
                                                                                                                                                                                                                                                                                                                                                                178 SITSHYK-PPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 DSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPG 123
                                                                                                                                                                                                                                                                  25 DKLQIGVKKRAENCVQKSRKGDQLHMHYTGTLLDGTEFDSSRTRNEEFTFTLGGGNVIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 MDEGLLGVCIGEKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVIDFHNPSDSI 177
               A;Infrons: 27/3; 116/2; 200/3
C;Superfamily: BKBP-type peptidylprolyl isomerase homology
F;52-98/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
F;166-213/Domain: BKBP-type peptidylprolyl isomerase homology <PPII>
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                                                                                                                                                                                        94; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 IAMDGMCEGERRRVVIPSEYGYGSOGSPPEIPGGARLFFEIVLEKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 MGLREMCVGEXRIVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.6%; Score 286.5; DB 2
48.7%; Pred. No. 1.7e-16;
ive 18; Mismatches 40
                                                                                                                                      th 14.3%; Score 301.5; DB 2
| Similarity 32.2%; Pred. Nov. 2.3e-17; 73; Conservative 45; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56; Conservative
                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: F36H1.1
A; Map position: 5
                                                                                                                                        Query Match
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A,Note: inhibited by immunosuppressant drugs FK506 and rapamycin C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase; C;Keywords: cis-trans-isomerase; cyclosporin A binding; immunoregulation E;1-22/Domain: signal sequence #status predicted <SIO: F;23-151/Product: peptidylprolyl isomerase FKBPIS #status predicted <MAT> F;49-96/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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C;Genetics:
A;Gene: FXBP15-2
C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomeras
C;Keywords: cis-trans-isomerase
F;52-99/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>>
Proc. Natl. Acad. Sci. U.S.A. 93, 6964-6969, 1996
A;Title: Molecular characterization of a FKBP-type immunophilin from higher plants.
A;Reference number: Z17411; MUID:96293457; PMID:8692927
A;Accession: T12090
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-151 <LUA>

    Arabidopsis thaliana

                                                                                                                                                                                                                         A;Cross-references: EMBL:U52045; NID:g1272409; PIDN:AAC49392.1; PID:g1272410 C;Genetics:
A;Gene: FKBP15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-2 - Arabidopsis thaliae NAlternate names: FK-binding protein 15-2; immunophilin C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 16-Jul-1999 C;Accession: S71238
R;Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.
Ridan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.
A;Bescription: Molecular characterization of a FKBP-type immunophilin from hA;Reference number: S71238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y18D10A.19b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 SSFERNSPIDFELGGGQVIKGWDQGLLGMCLGEKRKLKIPAKLGYGEQGSPPTIPGGATL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 SSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGR-GNIPGSAVL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 ISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 LVFDV-----ALLDLHNPKD--SISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 LQIGVKFKPKTCEVQAHKGDIIKVHYRGKLTDGTVFDSSFERGDPFEFKLGSGQVIKGWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151,
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QGLLGACVGEKRKLKIPAKLGYGEQGSPPTIPGGATLIFDTELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 269; DB 2; 42.1%; Pred. No. 5.3e-15; ive 24; Mismatches 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.6%; Score 265.5; DB 2 48.1%; Pred. No. 1.1e-14; ive 17; Mismatches 36
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es 56; Conserv
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A, Molecule type: mRNA
A, Residues: 1-163 < LUA>
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Best Local S:
Matches 56
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Best Local S
Matches 50
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F;1-18/Domain: signal sequence #status predicted csIGs.
F;19-311/Product: peptidylprolyl isomerase FKBP-33 #status predicted cMAT>
F;19-311/Product: BKBP-type peptidylprolyl isomerase homology cpPII>
F;224-271/Domain: BKBP-type peptidylprolyl isomerase homology cpPII>
F;24-271/Domain: BKBP-type peptidylprolyl isomerase homology cpPII>
F;19/Modified site: fatty acylated amino end (Cys) (covalent) #status predicted
F;19/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                    peptidylprolyl isomerase (EC 5.2.1.8) FKBP-33 precursor - Streptomyces chrysomallus peptidylprolyl isomerase (EC 5.2.1.8) FKBP-33 precursor - Streptomyces chrysomallus C; Species: Streptomyces chrysomallus C; Species: Streptomyces chrysomallus C; Accession: S4628 Step. 1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Accession: S4628 R; Pahl, A.; Keller, U. EMBO J. 13, 3472-3480, 1994 A; Release chrysomallus FKBP-33 is a novel immunophilin consisting of two F A; Reference number: S46227; MUID:94341259; PMID:8062824 A; Residues: S46227; MUID:94341259; PMID:8062824 A; Accession: S46227; MUID:9435270; PIDN:CAA84280.1; PID:g633644 A; Experimental source: ATCC 11523 C; Genetics:
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C;Date: (05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000 C;Accession: T12090
R;Luan, S.; Kudla, J.; Gruissem, W.; Schreiber, S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                                      236
                                                                                                                                        237 MGLREMCVGEKRIVIIPPHLGYGEAGVDGEVPGSAVLVPDIELLELV
                                                                                                                                                                  190 IAMDGMCEGERRRVVIPSEYGYGSQGSPPEIPGGARLFFEIVLEKLV
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                                                                          148 QIDQIHKIEADKCKKAEAGDKIYQQYVLRLEDNTL
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peptidylprolyl isomerase (EC 5.2.1.8) ROF1 - Arabidopsis thaliana
NyAlternate names: FR565-binding protein; immunophilin; rotamase
Cispecies: Arabidopsis thaliana (mouse-ar cress)
Cispecies: Arabidopsis thaliana (mouse-ar cress)
Cispecies: 72448; S72484
Rivucich, V.A.; Gasser, C.S.
Mol. Gen. Genet. 252, 510-517, 1996
A;Title: Novel structure of a high molecular weight FK506 binding protein from Arabi A;Reference number: S72484; MUID:97071666; PMID:8914512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allitrons: 62/1; 91/1; 178/1; 203/1; 230/1; 295/1; 326/1; 384/3; 425/3; 474/3; 517/2 C; Superfamily: peptidylprolyl isomerase ROFI; BKBP-type peptidylprolyl isomerase hom C; Keywords: calmodulin binding; cis-trans-isomerase homology cPPII> F; 57-104/Domain: BKBP-type peptidylprolyl isomerase homology cPPII> F; 77-3216/Domain: BKBP-type peptidylprolyl isomerase homology cPPII> F; 290-339/Domain: BKBP-type peptidylprolyl isomerase homology cPPI3> F; 449-447/Domain: tetratricopeptide repeat homology cTTI> F; 449-482/Domain: tetratricopeptide repeat homology cTT2> F; 483-516/Domain: tetratricopeptide repeat homology cTT3> F; 483-516/Region: calmodulin-binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isomeras
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A; Residues: 1-551 < VUC>
A; Residues: 1-551 < VUC>
A; Residues: 1-551 < VUC>
A; Cross-references: EMBL:U57838; NID:g1373395; PIDN:AAB82062.1; PID:g1373396
A; ANOte: the nucleotide sequence was submitted to the EMBL Data Library, May 1996
A; Accession: S72484
A; Status: nucleic acid sequence not shown
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A;Residues: 1-429, VV, 431-551 <VUM>
A;Cross-references: EMBL:U49453; NID:g1354206; PIDN:AAB82061.1; PID:g1354207
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X76006; NID:g435470; PIDN:CAA53594.1; PID:g435471
C;Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl
F;41-88/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                                          FK506-binding protein - Botryllus schlosseri
C;Species: Botryllus schlosseri
C;Dacession: J0-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: J70748; S40074
R;Pancer, Z.; Gershon, H.; Rinkevich, B.
Biochem. Bloophys. Res. Commun. 197, 973-977, 1993
A;Fille: CDNA cloning of a putative protochordate FK506-binding protein.
A;Reference number: J70748; MUID: 94092189; PMID: 7505578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 CERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEK 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 12.2%; Score 256.5; DB 1
I Similarity 52.7%; Pred. No. 4.8e-14;
49; Conservative 15; Mismatches 28
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30.9%; Pred. No. 8.9e-13;
tive 34; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 RRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 168
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A;Residues: 1-134 <PAN>
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C,Superfamily: BKBP-type peptidylprolyl isomerase; BKBP-type peptidylprolyl isomerase
C,Keywords: cis-trans-isomerase
F;45-92/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 EVIPGLDIGIPKWKVGEIATFHVSGKYGYGRAGFRGLIPRNASLTCKVRLF-----NC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITSHYK-----PPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGS 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 304;
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                                                                                                                                                                                                                                                                                                                                                                                              A Introns: 82/1; 148/3; 195/1; 262/3
C, Superfamily: BKBP-type peptidylprolyl isomerase homology
F;102-149/Domain: BKBP-type peptidylprolyl isomerase homology
F;216-263/Domain: BKBP-type peptidylprolyl isomerase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.4%; Score 262; DB 2; Length 30
32.3%; Pred. No. 5.3e-14;
tive 33; Mismatches 98; Indels
                                                                          A;Reference number: Z20226
A;Accession: T26538
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
R'Harris, B. submitted to the EMBL Data Library, December 1998
                                                                                                                                                                                                              A;Residues: 1-304 <WIL>
A;Cross-references: BMBL:AL034393; PI
A;Cross-rimental source: clone Y18D10A
C;Genetics:
A;Gene: CESP:Y18D10A.19b
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Matches 51
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129 LGVCIGEKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVIDFHNPSD------SI 177

102 KIWKKGENAVFIIPAELAYGESGSPPTIPANATLQFDVELLKWDSVKDICKDGGVFKKIL 161
                                                                          49 EGYETPEN-----GDEVEVHYTGTLLDGTKFDSSRDRATPFKFTLGGGQVIKGWDIGI 101
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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

April 26, 2003, 06:48:55 ; Search time 6.91662 Seconds (without alignments) 2326.688 Million cell updates/sec Run on:

US-09-225-502-8 2106 1 TYGBIGWLIPGMDKGLLGMC......VNDFPLKLLYFTNLNYFVLM 388 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q61576 mus musculu	Q43207 triticum ae	P45878 mus musculu	P32472 saccharomyc	P26885 homo sapien	O60046 neurospora	_	_		Q9scy2 arabidopsis		P27124 oryctolagus	P20081 saccharomyc	Q02790 homo sapien	-		_	P44760 haemophilus	P30416 mus musculu	P20071 homo sapien		-	P45523 escherichia		P26883 mus musculu	P39311 escherichia	_	3 xenopus 1	P97534 rattus norv	P26884 bos taurus	891	244	Q16645 homo sapien
SUMMARIES	ID	ă	FKB7 WHEAT	FKB2 MOUSE	FKB2_YEAST	FKB2 HUMAN	FK21 NEUCR	FKBP_NEUCR	FKB5_MOUSE	FKB5_HUMAN		FKBA_AERHY	FKB4 RABIT	FKBP_YEAST	FKB4 HUMAN	FKB1_DROME		FKB1_BOVIN		FKB4 MOUSE	FKB1_HUMAN	FKB1_RAT	FKBP NEIMA	FKBA_ECOLI	FKBP_NEIMB	FKB1 MOUSE		FKBA_BUCAI		FKBB RAT			FKB3_MOUSE	FKBB_HUMAN
	jth DB	581 1		•		141 1		•	456 1	• •	208 1	•		114 1		108 1	112 1	107 1	241 1	457 1	107 1	107 1	109 1	270 1	109 1	-	205 1		107 1			11	224 1	107 1
de	Query Match Length	5.	٦.	٥.	۳.		٦.	6.	۳.	۲.	۲.	٥.	٥.	6.	٥.	۰	9.	4.	4.	۳.		.2	٦.	٦.	٥.	٥.	∞.	∞.	9.	9.	9.	9.	7.6	7.6
	Score	1022	283.5	251	237.5	236.5	233.5	208.5	195	194	193	190	189	188	188	184.5	182	177	176	175	173	172	171.5	171.5	169.5	169	164.5	164	161	161	191	161		160
	Result No.	-	71	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	1,9	20	21	22	23	24	25	56	27	28	29	30	31	32	33

O46638 oryctolagus Q00688 homo sapien	P28725 streptomyce Q06205 saccharomyc P26623 chlamydia t	-		P42458 corynebacte Q26486 spodoptera	-
1 FKB3_RABIT 1 FKB3_HUMAN	1 FKBP_STRCH 1 FKB4_YEAST 1 MIP CHLTR	1 FKB4 DROME 1 FKBP_CANAL	1 FKB4 SCHPO 1 MIP_CHLPN	1 FKBP_CORGL 1 FKB4_SPOFR	1 MIP_CHLMU
223 224	124 392 243	357 124	361 258	118 412	243
7.5	7.2	6.9 6.9	6 4.4.	6.3 6.3	6.1
159	152.5 150.5 150	146 144.5	135.5 135	133 131	128
35 35	36 337 38	39 40	4 4 2 2 2	4 4 4	45

ALIGNMENTS	REBULT. FREX. MOUSE TEXA MOUSE TEXA MOUSE TEXA MOUSE TEXA MOUSE TEXA MOUSE TEXA MOUSE TO GRE1.39, Created) TO GA1576. TO GA1776.	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPIASE,
PPIASE,
PPIASE,
TPR 1.
TPR 2.
TPR 3.
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STRAIN=CV. ATIR; TISSUE=Root tip;
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hes 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517
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REPEAT
REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
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                                                                                                                                                                                                                                                                                               FINITE STATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 NPKDIYQLETLEIPQGCVRRAVAGDFMRYHYNGSLMDGTLFDSSYSRNHTYNTYVGQGYI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 KTLSRPPENCNETSKIGDFIRYHYNCSLLDGTRLFSSHDYEAPQEITLGANKVIEGLDRG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 TYIGSGWLIKGMDQGLLGMCPGEKRKIIIPPFLAYGEKGYGTVIPPQASLVFYVLLLDVH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                          Pram; Frvez, SMO054; EPh; 2.

PROSITE; SMO054; FRBP PPIASE 1; FALSE NEG.

PROSITE; PS00454; FKBP PPIASE 2; 1.

PROSITE; PS00045; FKBP PPIASE 3; 4.

PROSITE; PS00014; EF TÄRGET; 1.

PROSITE; PS00018; BF HAND; 1.

ISOmerase; Rotamase; Repeat; Glycoprotein; Signal; Phosphorylation; Taloniasmic reticulum; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGBGKDIPGQASLVFDVALLDLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 TSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPNLFERIN-----KVTFFCCPFVSWRRWYPEGRGQL-PQDSNDSPPADL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|||:::
501 STSLFEDWDLNKDGEVPPEEFSSFIKAQVN-----EGKGRLMPGQDFDKTISDM 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.5%; Score 1022; DB 1; Length 581; 55.8%; Pred. No. 3.1e-78; ive 58; Mismatches 79; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            559 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence
16-OCT-2001 (Rel. 40, Last annotati
70 kDa peptidylprolyl isomerase (Ec
                InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00036; efhand; 2.
Pfam; PF00254; FKBP; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64669 MW;
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InterPro; IPR000886; ER
                                                                                                                                                                                                                                                                                                      581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                      Matches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKB7 WHEAT Q43207;
                                                                                                                                                                                                                                                                                                 CHAIN
DOMAIN
DOMAIN
DOMAIN
CA_BIND
CA_BIND
CAEBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
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FKB7_WHEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 LRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPPHLG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGKDIPGQASLVFDVALLDL---HNPKDSISIENKVVPENCER-----ISQSGDF 86
197 --YLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTVIIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 YGEEGR-GNIPGSAVLVFDIHVIDFHNPSDSISITSHYKPPDCSVLSKKGD
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X86903; CAA60505.1; -.
HSSP; P27124; 1ROT.
InterPro; IPRO011179; FKBP_PPIase.
InterPro; IPRO01440; TFRP_
Pfam; PF00254; FKBP; 3.
Pfam; PF00258; TFR; 3.
SMART; SM00453; FKBP_PPIASE 1; 1.
PROSITE; PS00453; FKBP_PPIASE 2; 3.
PROSITE; PS00454; FKBP_PPIASE 2; 3.
PROSITE; PS00659; FKBP_PPIASE 2; 3.
ISOMETASE; NCATHMASE; REP_PPIASE 2; 3.
ISOMETASE; RCATHMASE; REP_PPIASE 2; 3.
ISOMETASE; RCATHMASE; REP_PPIASE 2; 3.
ISOMETASE; RCATHMASE; REP_PPIASE 3; 3.
ISOMETASE; RCATHMASE; REP_PPIASE 3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62056 MW; 5C5DAE70D716B541 CRC64;
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; Pred. No. 3.3e-16;
43; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKBP-TYPE 1
FKBP-TYPE 2
FKBP-TYPE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 32, Created)
(Rel. 32, Last sequence update)
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P45878;
01-NOV-1995 (
01-NOV-1995 (
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(FKBP-13) (FKBP-15) (Peptidyl-prolyl

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FK506-binding protein precursor
                                                                                                                                                                                             NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                             MEDLINE-94085790; PLANDE-LIVEL;
MEDLINE-94085790; PLANDE-LIVEL;
Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,
Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,
Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,
Hendrickson B.A., Zhang W., Craig R.J., Jin Y.J., Bierer R.E.,

Burakoff S.J., Dilella A.G.;

"Structural organization of the genef encoding human and murine
RK506-binding protein (RKBP) 13 and comparison to FKBP1.";

Gene 134:271-275(1993).

-I - FUNCTION: PPISSES accelerate the folding of proteins. May function
as a component of membrane cytoskeletal scaffols.

-I - GATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPPINED BONUS IN OLIGOPEPTIDES.

-I - ENYME REGULATION: INHIBITED PS BOTH FK506 AND RAPAMYCIN.

-I - SUBGULILIA LILETATION: BNDOPLASMIC RETICULUM LUMEN. MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 SISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 QIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIKGW 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59; Conservative 26; Mismatches 51; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LSWILT----ILSICLSA-----RKL 29
                                (FKBP-13) (Peptidyl-prolyl cis-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLHNPKD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FK506-BINDING PROTBIN.
PREVENT SECRETION FROM ER (POTENTIAL).
F4E7FCC7766A0416 CRC64;
                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 DEGLIGVCIGEKRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVIDFHNPSD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 251; DB 1; Length 140; 34.3%; Pred. No. 2.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M77831; AAA37631.1; -.
HSSP; P20081; IYAT.
MGD; MGI:95542; Fkbp2.
InterPro; IPR001179; FKBP PPIASE.
PROSITE; P800453; FKBP; 1.
PROSITE; P800454; FKBP PPIASE 1; 1.
PROSITE; P850059; FKBP PPIASE 2; 1.
PROSITE; P850059; FKBP PPIASE 3; 1.
ISOMETASE; ROLAMASE; 3; 1.
ISOMETASE; PS50059; FKBP PPIASE 3; 1.
ISOMETASE; PS50059; FKBP PPIASE 3; 1.
ISOMETASE; PS50059; FKBP PPIASE 3; 1.
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Last sequence update)
Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                FK506-binding protein precursor (1 isomerase) (PPiase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AA; 15344 MW;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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(Rel. 27, I
(Rel. 38, I
                                                                                                                         musculus (Mouse).
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                                                                                                                                                                                                         NCBI TaxID=10090;
                                                                                      FKBP2 OR FKBP13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993
01-OCT-1993
15-JUL-1999
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P32472;
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ش
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                                                                                                                                                                                                                                                             Ø
                                             Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                           Partaledis J.A., Fleming M.A., Harding M.W., Berlin V.; "Saccharomyces cerevisiae contains a homolog of human FKBP-13, membrane-associated FK506/rapamycin binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 135;
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                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 2; 1.
PROSITE; PS50059; FKBP PPIASE 3; 1.
SIGMEL 1 17 POTENTIAL.
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43.1%; Pred. No. 3.8e-13;
tive 22; Mismatches 41
(PPiase) (EC 5.2.1.8)
9W OR D9719.24.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 18-54. MEDLINE=92366483; Pubmed=1380159;
                                                                                                                                                                                                     MEDLINE=93070605; PubMed=1279908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P20081; 1YAT.
SGD; SG002927; FKB2.
InterErc; IPR001179; FKBP_PFlase.
Pfam; PF00254; FKBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M90646; AAA34604.1; -. EMBL; M90767; AAA34605.1; -. EMBL; U33057; ABB64960.1; -. PIR; S25337; S25337.
                  FPR2 OR FKB2 OR YDR519W OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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135 AA;
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                                      68 GSPIAFELGVGRVIKGWDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPPSADLVFDVE 127
                         108 NRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEG-RGNIPGSAVLVFDIH 166
                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FK506-binding protein precursor (FKBP-13) (Peptidyl-prolyl cis-trans isomerase) (Ppiase) (RC 5.2.1.8).
FKBP2 OR FKBP13.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93112052; PubMed=1281998; Dilella A.G., Hawkins A., Craig R.J., Schreiber S.L., Griffin C.A.; "Chromosomal band assignments of the genes encoding human FKBP12 and FKBP13.";
 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKS06-BINDING PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL).
STILAGSLSDL-----EIGIIKRIPVEDCLIKAMPGDKVKVHYTGSLLESGTVFDSSYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 189;819-823(1992).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMDIC PERTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
-!- SUBCELLUIAR LOCATION: ENDOPLASMIC RETICULUM LUMEN. MEMBRANE ASSOCIATED (PROBABLE).
-!- TISSUE SPECIFICITY: T-CELLS AND THYMUS.
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00254; FKBP; 1. PROSITE; PS00453; FKBP; 1. PROSITE; PS00454; FKBP PPIASE 1; 1. PROSITE; PS00454; FKBP PPIASE 2; 1. PROSITE; PS00059; FKBP PPIASE 3; 1. Incomerase; Rotamase; Signal; Endoplasmic reticulum; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                          TISSUB=Colon carcinoma;
MEDILMES91319747; PubMed=1713687;
Jin Y.-J., Albers M.W., Lane W.S., Bierer B.E., Schreiber S.L.,
Burakoff S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning of a membrane-associated human FK506- and rapamycin-binding protein, FKBP-13.";
Proc. Natl. Acad. Sci. U.S.A. 88:6677-6681(1991).
                                                                                                                                                                         141 AA.
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001179; FKBP_PPlase
                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M65128; AAA58473.1; -.
EMBL; M75099; AAA36563.1; -.
                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:3718; FKBP2.
MIM; 186946; -.
                                                                                                                                                                                                01-AUG-1992 (Rel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, JC1365, JC1365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q00688; 1PBK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
                                                                            167 VID 169
                                                                                              ::|
128 LVD 130
                                                                                                                                                                        FKB2 HUMAN P26885;
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13
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                                                                                                                                                                                                                                                63 KDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                       29 KLQIGVKKRV--DHCPIKSRKGDVLHMHYTGKLEDGTEFDSSLPQNQPFVFSLGTGQVIK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
FK506-BINDING PROTEIN.
PREVENT SECRETION FROM ER (POTENTIAL)
                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FKSG6-binding protein precursor (FKBP-21) (Peptidyl-prolyl cistrans isomerase) (Ppiase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.1%; Score 233.5; DB 1; Length 217; 46.4%; Pred. No. 1.5e-12; ive 15; Mismatches 36; Indels 1;
                                                                                                                                                                   DB 1; Length 141;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                               123 GMDEGLLGVCIGEKRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 168
                                                                                                                                                                                                                                                                                                                                                     GWDQGLLGMYEGEKRKLVIPSELGYGERGAPPKIPGGATLVFEVELL 133
                                                                                                                        9F4751CA7D82D064 CRC64;
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                                                                                                                                                              ; Score 236.5; DB 1;
; Pred. No. 4.9e-13;
18; Mismatches 36;
                                        r -> A.
/FTId=VAR_006411.
S -> TA.
/FTId=VAR_006410.
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HSSP; Q00688; 1PBK.
InterPro; IPR001886; ER target.
InterPro; IPR01179; FKBP_PPIase.
PROSITE; PS00453; FKBP; 1.
PROSITE; PS00454; FKBP_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE_2; 1.
PROSITE; PS000014; ER_TARGET; 1.
PROSITE; PS000014; ER_TARGET; 1.
                                                                                                      006412
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                                                                                 Y -> C.
/FTId=VAR
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                                                                                 96
21
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Best Local Similarity
Matches 45; Conserv
                                                                                                                          141 AA;
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                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=74-OR23-1A;
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21
                                        24
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                                                                                                                          SEQUENCE
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VARIANT
                                        VARIANT
                                                                                 VARIANT
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FK21 NEUCR
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81 LTIAPHLAYGNRAVGGIIPANSTLIFETELV 111
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REPEAT
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                                                                        064378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                   Tropschug M., Wachter E., Mayer S., Schoenbrunner E.R., Schmid F.X.; "Isolation and sequence of an FK506-binding protein from N. crassa which catalyses protein folding."; Nature 346:674-677(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 RISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRR 138
73 VPENCERISQSGDFLRYHYNGTL-LDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                  Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VPVBCDRKTRKGDKINVHYRGTLQSNGQQPDASYDRGTPFSFKLGGGQQVIKGWDEGLVDM 89
                                                                                                                                                                                                                                                                                                                                                                                                                            Nyakatura G., Mewes H.-W., Mannhaupt G.; Submitted (FBR-2001) to the EMBL/Genbank/DBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PERTIDS BONDS IN OLIGOPEPTIDES.
-!- SUBCELLULAR LOCATION: CYCOPIASMIC.
-!- MISCELLANEOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506.
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase) (PPiase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 AA; 13037 MW; AF97183C041563B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 9.9%; Score 204.5; DB 1; Similarity 44.0%; Pred. No. 8.9e-11; 40; Conservative 16; Mismatches 34;
                                                               Ä
                                                CIGEKRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 IVVPPHLGYGEEGRGN-IPGSAVLVFDIHVI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P18203; 1FKL.
InterPro; IPR001179; FKBP_PPIase.
Pfam, PP00254; FKBP, 1.
PROSITE; PS00453; FKBP_PPIASE 1; 1.
PROSITE; PS00454; FKBP_PPIASE 2; 1.
PROSITE; PS50059; FKBP_PPIASE 2; 1.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90348972; PubMed=1696687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL513463; CAC28766.1; -. PIR; S11090; S11090.
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                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                     Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=74-OR23-1A;
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                                                                                                                                  FKBP NEUCR P20080;
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Matches
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                                                                                                             RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
TISSUE SPECIFICITY: WIDELY EXPRESSED, HIGHEST LEVELS FOUND IN THE
LIVER, SKELETAL MUSCLE, KIDNEY AND THYMUS. EXPRESSION IS REGULATED
DURING ADIPOCYTE DIFFERENTIATION.
SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "FKBP51, a novel T-cell-specific immunophilin capable of calcineurin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOI. Cell. Biol. 15:4395-4402(1995).
-!- FUNCTION: INTERACTS WITH PROGESTERONE RECEPTOR (BY SIMILARITY)
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeh W.-C., Li T.-K., Bierer B.E., McKnight S.L., "I'dentification and characterization of an immunophilin expressed during the clonal expansion phase of adipocyte differentiation."; Proc. Natl. Acad. Sci. U.S.A. 92:11081-11085(1995).
                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
1-NOV-1997 (Rel. 35, Last sequence update)
51 kDa FKSO6-binding protein (FKBP51) (Peptidyl-prolyl cis-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE BONDS IN OLIGOPEPTIDES.
BNZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baughman G., Wiederrecht G.J., Campbell N.F., Martin M.M.,
Bourgeois S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 2; 1.
PROSITE; PS50059; FKBP PPIASE 3; 1.
ISOMERASE; RCTEMBE PPIASE 3; 1.
DOMAIN 165 251 PPIASE, FKBP-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8FD0C9B61478EB46 CRC64;
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:104670; Fkbp5.
InterPro; IPR001179; FKBP_PPIase.
InterPro; IPR00440; TPR.
Pfam; PF00254; FKBP; 2.
Pfam; PF00515; TPR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96074651; PubMed=7479941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95349606; PubMed=7542743;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c; TISSUE=Thymus;
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STANDARD;
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350
384
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                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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317
352
456 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                        FKBPS OR FKBPS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibition."
FKB5 MOUSE
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Length 456;

DB 1;

9.3%; Score 195;

Query Match

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Zhang J.S., Smith D.I.;
"Identification of AIG6 as an androgen response gene in human prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith D.F., Albers M.W., Schreiber S.L., Leach K.L., Deibel M.R. Jr.;
"FKBP54, a novel FK506-binding protein in avian progesterone receptor complexes and Hela extracts.",
J. Biol. Chem. 268:24270-2473(1993)
-!- FUNCTION: INTERACTS WITH FUNCTIONALLY MATURE HETERO-OLIGOMERIC PROGESTERONE RECEPTOR COMPLEXES ALONG WITH HSP90 AND P23.
-!- CATALYIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: INHIBITED BY FK506 BUT NOT CYCLOSPORIN.
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED, ENRICHED IN TESTIS COMPARED TO OTHER TISSUES.
                                                                                      194 KGDYLKYHYNASLLDGTLLDSTWNLGKTYN----IVLGSGQ---VVLGMDMGLREMCVG 245
                                                               GDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPP 143
                                                                                                                                         144 HLGYGEEGR-GNIPGSAVLVFDIHVIDFHNP---SDSISIT-----SHYKPPDCSVLSK 193
                                                                                                                                                                                                                                                   164 EGATVKVH-----LEGCC-----GGRIFDCRDVVFVVGEGEDHDIPIGIDKALVKWQRE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baughman G., Wiederrecht G.J., Chang F., Martin M.M., Bourgeois S., "Tissue distribution and abundance of human PKBP51, an PK506-binding protein that can mediate calcineurin inhibition."; Biochem. Biochem. Biochem. 232:437-443(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 9-457 FROM N.A.

MEDLINE=97154494; PubMed=9001212;

Nair S.C., Edimerman R.A., Toran E.J., Chen S., Prapapanich V.,

Butts R.N., Smith D.F.;

"Molecular cloning of human FKBP51 and comparisons of immunophilin interactions with Hsp90 and progesterone receptor.";

Mol. Cell. Biol. 17:594-603(1997).
                                                                                                                                                                           110 EYAYGSAGHLOKIPSNATLFFEIELLDFKGEDLFEDSGVIRRIKRKGEGYSNPN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
51 kDa FK506-binding protein (FKBPS1) (Peptidyl-prolyl cis-trans isomerase) (RC 5.2.1.8) (Ppisae) (Rotamane) (54 kDa progesterone receptor-associated immunophilin) (FKBPS4) (FR1 antigen)
(HSP90-binding immunophilin) (Androgen-regulated protein 6).
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer cell line LNCaP.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
7e-09;
80;
       29.8%; Prec. ...
                                                                                                                                                                                                                                                                                       246 EKRTVIIPPHLGYGEAGVDG-EVPGSAVLVFDIEL 279
                                                                                                                                                                                                                                                                                                                213 BQCILYLGPRYGFGBAGKPKFGIDPNAELMYEVTL 247
                                                                                                                                                                                                                                                                                                                                                                                                             457 AA.
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TISSUE=Thymus;
MEDLINE=97242207; PubMed=9125197;
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Mammalia; Eutheria; Primates;
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [4]
CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                   FKB5 HUMAN Q13451;
             Local
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15-00N-2002 (Rel. 41, Last annotation update)
15-00N-2002 (Rel. 41, Last annotation update)
15-00N-2002 (Rel. 41, Last annotation update)
15-00N-2002 (Rel. 41, Last annotation update)
15-00N-2002 (Rel. 41, Last annotation update)
15-00N-2002 (Rel. 41, Last annotation update)
15-00N-2002 (Rel. 41, Last annotation update)
16-00N-2002 (Rel. 41, Last annotation update)
17-00N-2002 (Rel. 41, Last annotation update)
18-00N-2002 (Rel. 41, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 DIHNPKDS--ISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------KGEDL-----FEDGGIIRRTKRKGEGYSNPNEGATVEIH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 LEGRCGGRMFDCRDVAFTVGEGEDHDIPIGIDKALEKMQREEQCILYLGPRYGFGEAGKP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 GQGYVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVIDFHNPS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IVLGSGQ---VVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 DITSKKDRGVLKIVKRV--GNGEETPMIGDKVYVHYKGKLSNGKKFDSSHDRNEPFVFSL
  INDUCTION: By androgen. SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 DSISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, Frons Front, 2.
Pfam, PF00515; TPR; 2.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00454; FKBP PPIASE 2; 1.
PROSITE; PS50059; FKBP PPIASE 3; 1.
PROSITE; PS50059; FKBP PPIASE 3; 1.
Tormerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18A86608C6891A73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 194; DB 1;
26.1%; Pred. No. 8.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Mismatches
                                                     FKBP-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 TPR REPEATS.
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TPR 2.
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Interpro; IPRO0140; TPR.
Pfam; PF00254; FKBP; 2.
Pfam; PF00515; TPR; 2.
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EMBL; AF194172; AAL54872.1; -
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Genew; HGNC:3721; FKBP5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 KFGIEP-NAELIYEVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GEVPGSAVLVFDIEL
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157
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317
352
457 AA;
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Best Local Similarity
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Q9SCY2;
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FKB3_ARATH
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154 ----NIPGSAVLVFDIHVI 168
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Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;
Submitted (JAN-2000) to the SWISS-PROT data bank.
-!- FUNCTION: PPIases accelerate the folding of proteins. It catalyzes
the cis-trans isomerization of proline imidic peptide bonds in
    oligopeptides (By similarity).
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||| BSYNRGKPLTFRIGVGEVIKGMDQGILGSDGIPPMLTGGKRTLRIPPELAYGDRGAGCK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSSYSRNRTFDTYIGQGYVIPGMDEGLLG-----VCIGEKRRIVVPPHLGYGEEGRG-- 153
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                                                                                                                                                                      Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis full length cDNA clones (RAFLs) sequenced by SSP consortium (Salk/Stanford/PGEC).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones.";
DNA Res. 5:203-216(1998).
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Kolukisaoglu U., Billion K., Eckhoff A., Moeller A., Saal B.,
Wanke D., Schulz B.;
"Structure and evolution of FKBP-like genes in Arabidopsis.";
Structure (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001179; PKBP_PPlase.
Pfam, PF00254; FKBP_PPLASE.
PROSITE; P800454; FKBP_PPLASE.
PROSITE; P800454; FKBP_PPLASE.
PROSITE; P80059; FKBP_PPLASE.
PROSITE; P800659; FKBP_PPLASE.
PROSITE; P850659; FKBP_PPLASE.
CHLOROPLAST (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANS ISOMERASE 3.
4E6640FE7955A48F CRC64;
                                                                                               STRAIN=cv. Columbia;
MEDLINE=98403884; PubMed=9734815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB012245; BAB09210.1; -. EMBL; AY065047; AALS7682.1; -. EMBL; AJ242483; CAB64723.1; -.
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208
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                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wong C.Y.F., Heuzenroeder M.W., Quinn D.M., Flower R.L.P., "Cloning and characterization of two immunophilin-like genes, ilph and fkpA, on a single 3.9-kilobase fragment of Aeromonas hydrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 DFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPPH 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic DNA.";
J. Bacteriol. 179:3397-3403(1997).
J. Bacteriol. 179:3397-3403(1997).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. FKPA PROBABLY ACTS IN THE FOLDING OF EXTRACYTOPLASMIC PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE PKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKPA.
                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FKBP-type peptidyl-prolyl cis-trans isomerase fkpA precursor
                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 268;
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43.3%; Pred. No. 9.1e-09;
tive 14; Mismatches 35; Indels
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28685 MW; 5E88D74A830BE3FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRR000774; FKBP Nterm.
InterPro; IPR001774; FKBP Nterm.
InterPro; IPR001179; FKBP PPIASE.
Pfam; PF00264; FKBP; 1.
ProDom; PF001346; FKBP N; 1.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00654; FKBP PPIASE 2; 1.
PROSITE; PS50059; FKBP PPIASE 2; 1.
ROGITE; PS50059; FKBP PPIASE 2; 1.
ROGITE; PS50059; FKBP PPIASE 3; 1.
ROGITE; PS50059; FKBP PPIASE 3; 1.
ROGITE; PS50059; FKBP PPIASE 3; 1.
ROGITE; PST00858; PCBP PPIASE 3; 1.
      268 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97315206; PubMed=9171380;
                                                                                                                                                                                                          (PPiase) (Rotamase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U56832; AAC45362.1; -. HSSP; P20071; 1FKJ.
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hes 39; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257
                                                                                                                                                                                                                                                                      Aeromonas hydrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=644;
                                                                                                                                                                                                          5.2.1.8)
FKBA AERHY
008437;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PHOSPHORYLATION BY CK2.

MEDLINE=98070781; PubMed=9405642;

Miyata Y., Chambraud B., Radanyi C., Leclerc J., Lebeau M.-C.,

Renoix J.-M., Shirai R., Catelli M.-G., Yahara I., Baulieu E.-E.;

"Phosphorylation of the immunosuppressant FK506-binding protein FKBF52
by casein kinase II: regulation of HSP90-binding activity of FKBF52.";

Proc. Natl. Acad. Sci. U.S.A. 94:14500-14505(1997).
                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
FKS06-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase
FKBP4) (EC 5.2.1.8) (PPlase) (Roteamase) (R59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katze J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96374215; PubMed=8780506;
Crasscu C.T., Rouviere N., Popescu A., Cerpolini E., Lebeau M.-C.,
Baulieu E.-E., Mispelter J.;
"Three-dimensional structure of the immunophilin-like domain of
FRBPS) in solution.";
Biochemistry 35:11045-11052(1996).
-!- FUNCTION: Component of unactivated mammalian steroid receptor
complexes that sediment at 8-10 S. May have a rotamase activity.
May play a role in the intracellular trafficking of hetero-
oligomeric forms of steroid hormone receptors.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Immunophilins, refsum disease, and lupus nephritis: the peroxisomal enzyme phytanoyl-COA alpha-hydroxylase is a new FKBP-associated
                                                                                                                                                                                                                                                                                                                                                                                                                           "PS9, an hsp 90-binding protein. Cloning and sequencing of its cDNA and preparation of a peptide-directed polyclonal antibody."; J. Biol. Chem. 267:4281-4284 (1992).
                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92335279; PubMed=1631118;
Callebaut I., Renoir J.-M., Lebeau M.-C., Massol N., Burny A.,
Baulieu E.-E., Mornon J.-P.;
"An immunophilin that binds M(r) 90,000 heat shock protein: main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chambraud B., Radanyi C., Camonis J.H., Rajkowski K., Schumacher
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92165768; PubMed=1537818;
Lebeau M.-C., Massol N., Herrick J., Faber L.E., Renoir J.-M.,
Radanyi C., Baulieu E.-E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=New Zealand white; TISSUE=Liver;
BEDLINE=96154240; PubMed=8579355;
Deshpande K.L., Seubert P.H., Tillman D.M., Farkas W.R., K
"Cloning and characterization of CDNA encoding the rabbit
TRNA-guanine transglycosylase 60-kilodalton subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structural features of a mammalian p59 protein.",
Proc. Natl. Acad. Sci. U.S.A. 89:6270-6274(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 96:2104-2109(1999)
                                          457 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. 326:1-7(1996)
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99162565; PubMed=10051602;
                                                                                 Created)
                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH PHYH.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-25.
                                                                                                                                                                                                                                                                                     NCBI_TaxiD=9986;
                                                                                                                                                                                                                FKBP4 OR P59.
                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                             01-AUG-1992
                                      FKB4 RABIT P27124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baulieu E.
                                                                                                                                                                                            (FKBP59
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 GDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 EYAYGSAGSPPKIPPNATLVFEVELFEFKGEDLTDDEDGGIIRRIRTRGEGYARPNDGAI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 GDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDLGKGEVIKAWDIAVATMKVGELCRITCKP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 HLGYGEEGR-GNIPGSAVLVFDIHVIDFH-----NPSDSISI-----TSHYKPPDCSV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Gaps
    steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 LSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQ---VVLGMDMGLREMCVGEK
              hormone receptor complexes. Also interacts with peroxisomal phytamoyl-coA alpha-Pydroxylase (PHYH) (By similarity).
SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
PTM: Phosphorylation by CK2 results in loss of HSP90 binding
    unactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0454; FKBP PPIASE 1; 1.
PROSITE; PSO0454; FKBP PPIASE 2; 2.
PROSITE; PS50059; FKBP PRIASE 3; 2.
ISOMERABE; PS50089; FKBP PRIASE 3; 2.
ISOMERABE; Rotamase; TPR repeat; Repeat; Nuclear protein; 3D-structure; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89; Indels
                                                                                     SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS. SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECS8CC4BCF66A44A CRC64;
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TPR 2.
TPR 3.
PHOSPHORYLATION (BY CK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 %
 SUBUNIT: Associates with HSP90 and HSP70 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , DB 1;
2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKBP-TYPE
FKBP-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I (IN REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 2.2e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: | :: | | ::: | 218 STAFGNAGKEKFQIPPYAELKYEVHL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 RTVIIPPHLGYGEAGVDG-EVPGSAVLVFDIEL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S -> H (IN
EG -> FI (
S -> T (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPIASE,
PPIASE,
                                                                                                                                                                                                                                                                                                    PIR, A42386; A42386.
PDB, 1RCT, 07-DEC-96.
PDB, 1RCU; 07-DEC-96.
InterPro; IPR001179; FKBP PPIase.
InterPro; IPR001440; TPR.
Pfam; PP00254; FKBP; 2.
Pfam; PP00554; TPR; 3.
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                                                                                                                                                                                                                                                                         EMBL; M84474; AAA31438.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.2%;
                                                                                                                                                                                                                                                                                         M84988; AAA31439.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137
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14
20
25
457 AA;
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INIT MET
DOMAIN 49
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P20081;
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REPEAT
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FKBP_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic.
MISCELLANBOUS: FKBP BINDS TO THE IMMUNOSUPPRESSANT DRUG FK506 AND ALSO MEDIATES THE SENSITIVITY TO RAPAMYCIN.
SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                             "FKB1 encodes a nonessential FK 506-binding protein in Saccharomyces cerevisiae and contains regions suggesting homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91065908; PubMed=1701173; Siekierka J.J., Widerrecht G., Greulich H., Boulton D., Hung S.H.Y., Siedin J., Hodges P.J., Sigal N.H.; "The cytosolic-binding process for the immunosuppressant FK-506 is both a ubiquitous and highly conserved peptidyl-prolyl cis-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91141524; PubMed=1996117;
Koltin Y., Faucette L., Bergsma D.J., Levy M.A., Cafferkey R.,
Koser P.L., Johnson R.K., Livi G.P.;
"Rapamycin sensitivity in Saccharomycs cerevisiae is mediated by a peptidyl-prolyl cis-trans isomerase related to human PK506-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mallet L., Bussereau F., Jacquet M.;
"A 43.5 Kb segment of yeast chromosome XIV, which contains MFA2,
"MFP2, CAP/SRV2, NAM9, FKB1/FPR1/FBP1, MOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crystallographic and functional analysis.";
J. Biol. Chem. 268:7607-7609(1993).

-I. FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
-I. CATALYTIC ACTIVITY: C15-TRANS ISOMERIZATION OF PROLINE IMIDIC PERTIDE BONDS IN OLIGOPEPTIDES.
(PPiase) (EC 5.2.1.8) (Rapamycin-binding protein).
FPRI OR FKBI OR RBPI OR YNL135C OR N1213 OR N1845.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=93216714; PubMed=7681823;
Rotonda J., Burbaum J.J., Chan H.K., Marcy A.I., Becker J.W.;
"Improved calcineurin inhibition by yeast FKBP12-drug complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91156723; PubMed=1705713;
Heitman J., Movya R.N., Hiestand P.C., Hall M.N.;
"FK 506-binding protein proline rotamase is a target for the immunosuppressive agent FK 506 in Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 88:1948-1952(1991).
                                                                                                                                                                                                    MEDLINE=91126049; PubMed=1704127;
Wiederrecht G.J., Brizuela L., Elliston K.O., Sigal N.H.,
                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 88:1029-1033(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 265:21011-21015(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Cell. Biol. 11:1718-1723(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96109932; PubMed=8619318;
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                        Siekierka J.J.;
                                                                                                                                                                                                                                                                                                                                         cyclophilins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C
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EMBL; Z46843; CAA86890.1; -.

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Q02790; Q9UCV7, Q9UCP1;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
FKSO6-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase
FKBP4) (EC 5.2.1.8) (PPiase) (Rotamase) (p59 protein) (HSP binding
immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 VIDFHNPSDSISITSHYKPPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVL 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VIEGNVKIDRIS-----PGDGATFPKTGDLVTIHYTGTLENGQKFDSSVDRGSPFQCNI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 GSGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93066366; PubMed=1279700;
Peattie D.A., Harding M.W., Fleming M.A., Decenzo M.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12158 MW; 65C134830D300C06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%; Score 188; DB 1;
36.2%; Pred. No. 4.4e-09;
tive 22; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 AA
                                                                                                                                                       PS00453; FKBP_PPIASE 1; 1.
PS00454; FKBP_PPIASE 2; 1.
PS50059; FKBP_PPIASE 3; 1.
                                                                                                                                                                                            Isomerase, Rotamase, 3D-structure.
STRAND 3 4
                                                                                                                                 InterPro; IPR001179; FKBP_PPlase.
             AAA34607.1;
AAA34962.1;
CAA96017.1;
M57967; AAA03564.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                PIR, A33146, A33146.
PIR, A37870, A37870.
PIR, A39122, A39122.
PIR, C38333, C38333.
PIR, S13758, S13758.
PDB, 1YAT, 31-OCT-93.
SGD, S0005079, FPR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                            Pfam; PF00254; FKBP;
PROSITE; PS00453; FK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WCBI_TaxID=9606;
                                                                                                                                                                                                                                 M60877;
M63892;
                                     Z71411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
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                                                                                                                                                                    PROSITE;
PROSITE;
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STRAND
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FKB4_HUMAN
                                   EMBL;
                         EMBL;
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TURN
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Lippke J.A., Livingston D.J., Benasutti M.;
"Expression and characterization of human FKBF52, an immunophilin that associates with the 90-kDa heat shock protein and is a component of steroid receptor complexes.";
Proc. Natl. Acad. Sci. U.S.A. 89:10974-10978 (1992).
                                                                                                                                                                                                                 MEDLINE=92285692; PubMed=1376003;
Tai P.-K.K., Albers M.W., Chang H., Faber L.E., Schreiber S.L.;
"Association of a 59-kilodalton immunophilin with the glucocorticoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE BONDS IN OLIGOPEPTIDES.
SUBUNIT: Associates with HSP90 and HSP70 in unactivated steroid
                                                                                                                                                                                                                                                                                                                                       TISSUB=Lymphocytes;
MEDLINE=9033521; PubMed=2378870;
Sanchez B.R., Faber L.B., Henzel W.J., Pratt W.B.;
Sanchez B.R., Faber L.B., Henzel W.J., Pratt W.B.;
The 56-59-kilodalton protein identified in untransformed steroid
receptor complexes is a unique protein that exists in cytosol in a
complex with both the 70- and 90-kilodalton heat shock proteins.";
Biochemistry 29:5145-5152(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hormone receptor complexes. Also interacts with peroxisomal phytanoyl-coA alpha-hydroxylase (PHYH).
SUBSCILULMAR LOCATION: Nuclear and cytoplasmic.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
PTM: Phosphorylation by CK2 results in loss of HSP90 binding
                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-20, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION
                                                                                                                                    Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity (By similarity).
--- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMI---- SIMILARITY: CONTAINS 2 FKBP-TYPE PPIASE DOMAINS.
--- SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                                                                                   SEQUENCE OF 1-24, SUBUNIT, AND FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92147620; PubMed=1371107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPRO01179; FKBP_PPIase.
Interpro; IPRO01140; TPR.
Pfam; PP00254; FKBP; 2.
Pfam; P200515; TPR; 3.
                                                                                                                    TISSUE=Lung, Lymph, and Uterus;
Strausberg R.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC001786; AAH01786.1; --
EMBL; BC002887.1; --
EMBL; BC007924; AAH07924.1; --
PIR; A46372; A46372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M88279; AAA36111.1; -.
                                                                                                                                                                                                                                                                                      Science 256:1315-1318(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:3720; FKBP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P27124; 1ROT
                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        receptor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissum=T-cell;
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                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                      49 GDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDLGKGEVIKAWDIAIATMKVGEVCHITCKP 108
                                                                                                                                                                                                                                                                                                                                                                      144 HLGYGEEGR-GNIPGSAVLVFDIHVIDFH-----NPSDSISI-----TSHYKPPDCSV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                           169 VEVA---LEGYYXDKILFDQREL--RFEIGEGENL----DLPYGLERAIQRMEKGEHSIV 218
                                                                                                                                                                                                                                                                                                              84 GDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 EYAYGSAGSPPKIPPNATLVFEVELFEFKGEDLTEEEDGGIIRRIQTRGEGYAKPNEGAI
                                                                                                                                                                                                                                                                                                                                                                                                                            191 LSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMDMGLREMCVGEKRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
12 KDa FKS06-binding protein (FKBP) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (EC 5.2.1.8) (Macrolide binding protein).
DR PROSITE; PS00453; FKBP PPIASE 1; 1.

DR PROSITE; PS00454; FKBP PPIASE 2; 2.

PROSITE; PS00059; FKBP PPIASE 2; 2.

KW, Isomerase; Rotamase; Repeat; TPR repeat; Nuclear protein;

T NIT MET 0 0 0

T DOMAIN 49 137 PPIASE; FKBP-TYPE 1.

I DOMAIN 166 252 PPIASE; PKBP-TYPE 1.
                                                                                                                                                                                                             ED -> AR (IN REF. 2; AAH02887)
916B3B945C51634E CRC64;
                                                                                                                                                                                                                                                         Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                  92;
                                                                                                                                                                                                                                                        8.9%; Score 188; DB 1;
27.6%; Pred. No. 2.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA.
                                                                                                                                                                                                                                                                     Pred. No. 2.7e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 IIPPHLGYGEAGVDG-EVPGSAVLVFDIEL 279
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                                                                                                                                                       TPR
TPR
TPR
                                                                                                                                                                                                                            51673 MW;
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                                                                                                                                                                                                                                                                     27.6%;
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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1137
2552
3302
3351
142
146
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FK506-BP2 OR FKBP12.
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269
318
353
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145
458 AA;
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P48375;
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CONFLICT
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.8%; Score 184.5; DB 1; Length 108; Best Local Similarity 37.8%; Pred. No. 8.1e-09; Matches 37; Conservative 19; Mismatches 41; Indels 1.
                                      EMBL; Z49079; CAA88904.1; -.
EMBL; U41441; AAA91178.1; -.
HSSP; P18203; 1FKL.
RIYBase; FBgm0013954; FK506-bp2.
InterPro; 1PR001179; FKBP_PP188e.
Pfam; PF00254; FKBP; 1.
PROSITE; PS00453; FKBP; PP1ASE_1; 1.
PROSITE; PS50053; FKBP_PP1ASE_2; 1.
PROSITE; PS50059; FKBP_PP1ASE_2; 1.
PROSITE; PS50059; FKBP_PP1ASE_3; 1.
SEQUENCE 108 AA; 11597 MW; 48BCF993ACBD350A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           132 CIGEKRRIVVPPHLGYGEEGR-GNIPGSAVLVFDIHVI 168
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68 SVGQSAKLICSPDYAYGSRGHPGVIPPNSTLTFDVELL 105
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Search completed: April 26, 2003, 06:56:22 Job time : 8.91662 secs

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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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April 26, 2003, 06:48:54; Search time 34.1369 Seconds (without alignments) 2341.934 Million cell updates/sec Run on:

Title: Perfect score: Seguence:

US-09-225-502-8 2106 1 TYGEIGWLIPGMDKGLLGWC......VNDFPLKLLYFTNLNYFVLM 388

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp archea:*
sp_bacteria:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_phage:*
sp_phage:*
sp_prage:*
sp_prage:*
sp_vortebrate:*
s SPTREMBL 21:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	O95302 homo sapien O92247 mus musculu O87386 mus musculu O891878 sallus gall O91878 senopus lae O84411 mus musculu Q94613 homo sapien Q94631 homo sapien Q94631 homo sapien Q94631 homo sapien Q94631 homo sapien Q94639 homo sapien Q94639 caenorhabdi P91180 caenorhabdi Q95460 caenorhabdi
SUMMARIES	095302 095302 087336 087336 091878 087111 091878 091873 091873 091809 091809 091809 095060
DB	
% Query Aatch Length DB	517 570 570 570 581 581 582 582 582 582 582 582 582 583 583 583 583 583 583 583 583 583 583
% Query Match	1.00 4 4 4 4 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1
Score	1585 1585 1585 1069.5 1000.5 1
Result	2 4 5 9 5 7 8 6 7 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 9 7 8 8 9 9 8 9 9 9 9

Q9v3v2 drosophila Q20107 caenorhabdi Q9xz54 drosophila Q9xgx3 drosophila Q9fjl3 arabidopsis Q966y5 suberites d	Q53919 streptomyce Q41649 vicia faba Q9fjl2 arabidopsis Q9wWG caenorhabdi Q38935 arabidopsis	Q91sf4 arabidopsis Q17280 bocryllus s Q38931 arabidopsis Q38949 arabidopsis Q91sf3 arabidopsis Q018f3 arabidopsis	Q9bts7 homo sapien 096335 brugia mala 09rwm8 homo sapien Q9df18 gillichthys Q9cre4 mus musculu 09v6b0 homo sapien	homo 7 mus homo
Q9V3V2 Q20107 Q9XZ54 Q9VGK3 Q9FJL3 Q9FJL3	Q53919 Q41649 Q9FJL2 Q38936 Q9XW05 Q38935	Q9LSF4 Q17280 Q38931 Q38949 Q9LSF3 Q04843	Q9BTS7 Q96335 Q9NWM8 Q9DFL8 Q9CRE4	Q96DA4 Q9D8P8 Q9D1M7 Q9NYL4 Q9HXS4
	22222	100100	4 1 1 3 4 6 4 6	4 11 11 16
216 139 216 138 578 509	312 151 163 304 146	153 134 551 551 555	142 137 211 119 122	222 189 201 201 113
13.6 13.6 13.0 12.9	12.6 12.6 12.6 12.6 12.6	12.3 11.3 11.9 11.9	11.8 11.3 10.8 10.7	10.7 10.6 10.6 10.5
286.5 285 285 275 274 274	269 265 265 265 262 259	256.5 251.5 251.5 251.5 251.5	247.5 234.5 227.5 225.5	225 223.5 223.5 221.5 214.5
11 118 22 22 22	22 2 2 2 2 4 2 2 2 3 4 2 3 4 2 4 3 4 3 4		* 	4 4 4 4 4 4 5 6 4 5

ALIGNMENTS

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MGD; MGI:1350921; Fkbp9.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q92247 PRELIMINARY, PRT; 570 AA.
Q92247, Q92HXS; Q9CVM0;
Q012A47-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2092 (TrEMBLrel. 20, Last annotation update)
FKS06 binding procein 9 precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (FKBP65RS).
                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 IPGMDEGLLGVCIGERRRIVVPPHLGYGEEGRGNIPGSAVLVFDIHVIDFHNPSDSISIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHYKPPDCSVLSKKGDYLKYHYNASILDGTLLDSTWNLGKTYNIVLGSGQVVLCMDMGIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I PGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGNI PGSAVLVFDIHVIDFHNPSDSISIT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SIS -> HEG (IN REF. 2; AAH07443).
H -> Q (IN REF. 2; AAH11872).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.1%; Score 1623; DB 4; Length 517; 99.0%; Pred. No. 5.6e-130; ive 1; Mismatches 2; Indels
                                                                                                                                                                                              PROSITE; PS50059; PKBP_PPIASE 3; 4.
Isomerase; Rotamase; Repeat; Glycoprotein; Phosphorylation;
Endoplasmic reticulum; Calcium-binding.
                                                                                                                                                                                                                                                                       PPIASE, FKEP-TYPE 1.
PPIASE, FREP-TYPE 2.
PPIASE, FKEP-TYPE 3.
PPIASE, FKEP-TYPE 4.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
PREVENT SECRETION FROM ER (1)
                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
             InterPro; IPR002048; EF-hand.
InterPro; IPR001179; FKEP_PPIase.
InterPro; IPR001179; FKEP_PPIase.
InterPro; IPR001179; FKEP_PPIase.
Pfam; PF00254; FKBP; 4
SMART; SM00054; EFH; 2.
PROSITE; PS00018; EF HND; 1.
PROSITE; PS00454; ERP_PPIASE 1; PALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE 2; 3.
PROSITE; PS00454; FKBP_PPIASE 2; 4.
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                                                                                                                                                                                                                                      Endoplasmic reticulum;
NON_TER 1 1
DOMĀIN 1 86
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216
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Matches 305;
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CONFLICT
SEQUENCE
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DOMAIN
CA BIND
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SEQUENCE OF 155-570 FROM N.A.

SEQUENCE OF 155-570 FROM N.A.

STRAIN-C57BL/63; TISSUE=PRNCREAS;

KARAIN-C57BL/63; TISSUE=PRNCREAS;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Radchi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Alzawa K., Izawa M., Nishi K., Kiyosawa T., Saito R.,

Asito T., Okazaki Y., Gojobori T., Bono H., Batalov S., Casavant T.,

Radcta K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radcta K., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,

Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Hayashizaki Y.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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R InterPro; IPR0010886; ER target.

InterPro; IPR001179; FKBP PPIase.

Pfam; PF00036; efhand, 2.

R Pfam; PF00036; efhand, 2.

R Pfam; PF00036; EF HAD; 1.

R PROSTTE; PS00018; EF HAND; 1.

R PROSTTE; PS00045; FKBP PPIASE 1; PALSE_NEG.

R PROSTTE; PS00059; FKBP PPIASE 2; 3.

R PROSTTE; PS0059; FKBP PPIASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=THYMUS;
PubMed=11710534;
Jo D., Lyu M.S., Cho E.-G., Park D., Kozak C.A., Kim M.G.;
Jo Dot, Lyu M.S., Cho E.-G., Park D., Kozak C.A., Kim M.G.;
Identification and genetic mapping of the mouse Fkbp9 gene encoding a new member of FKE96-binding protein family.";
Mol. Cells 12:272-275(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- ENZYME REGULATION: INHIBITED BY FKSO6.
-!- SUBCELLULAE LOCATION: ENDOPLASMIC RETICULUM.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, SKELETAL.
-!- TISSUE, LUNG, LIVER AND KIDNEY. LOWER LEVELS FOUND IN BRAIN,
                                                                                                                                                                                                                                  U., Krauss of the FKPB
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-i- PTM: PHOSPHORYLATED.
-i- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
SEQUENCE FROM N.A., ENZYME REGULATION, SUBCELLULAR LOCATION, TI
SPECIFICITY, DEVELOPMENTAL STAGE, AND CALCIUM-BINDING ACTIVITY.
MEDLINE-99453729; Pubble A. S. Seternes O.M., Moens U., Kraus
Shadidy M., Caubit X., Olsen R., Seternes O.M., Moens U., Kraus
"Biochemical analysis of mouse FKBP60, a novel member of the Fi
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--- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
EMBL; AF090334; AAC72964.1; --
EMBL; AF79263; AAF79215.1; --
EMBL; AK007499; BAB25071.1; --
HSSP; P20081; 1YAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1446:295-307(1999).
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MEDLINE=98384310; PubMed=9716519;
WEDLINE=98384310; PubMed=9716519;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                            61 NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120
                                                                                                                                                                                                                                                                                                                                                                                                   315 IPGMDEGLLGVCIGERRRIVVPPHLGYGEKGRGSIPGSAVLVFDIHVIDFHNPSDSISIT 374
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                                                                                                                                                                                                                                                                              255 NPKDTISIENKVVPENCERRSQSGDFLRYHYNGTLLDGTLFDSSYSRNHTFDTYIGQGYV
                                                                                                      TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH
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                                            Indels
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                                            4
          Pred. No. 1.1e-126;
9; Mismatches 4;
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          95.88;
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                                         295; Conservative
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          Similarity
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          Best Local
Matches 29
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Q9YIC3;
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FRSO6 binding protein 9.

Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1585, DB 11; Length 570;
Pred. No. 1.1e-126;
9; Mismatches 4; Indels 0
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G -> S (IN REF. 3).
A -> T (IN REF. 3).
V -> F (IN REF. 3).
V -> F (IN REF. 2).
F -> V (IN REF. 2).
F -> V (IN REF. 2).
S -> I (IN REF. 2).
S -> I (IN REF. 2).
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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                        PPIASE, FKBP-TYPE 1.
PPIASE, FKBP-TYPE 2.
PPIASE, FKBP-TYPE 3.
PPIASE, FKBP-TYPE 3.
PPIASE, FKBP-TYPE 3.
PF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
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Last annotation update)
FK506 BINDING PROTEIN
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01-UUN-2002 (TrEMBLrel. 21, Last seqn
01-JUN-2002 (TrEMBLrel. 21, Last senn
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G -> S
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Best Local Similarity 95.8%;
Matches 295; Conservative
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475
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570 AA;
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495 NLFERIDR 502
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Q8R386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435
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61 NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120
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      240 REMCVGEKRIVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEVS 299
                                         426 LGMCVGERRTVLVPPHLAHGESGARG-VPPSAVLKFDLELLHIEEGIPDGYLFIMLODTP 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 NPKDTVQLETLELPQGCVRRAVAGDFMRYHYNGSLMDGTLFDSSYSRNHTYNTYVGQGYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SVJ;

A Patterson C.E., Gao J., Rooney A.P., Davis B.C.;

Patterson C.E., Gao J., Rooney A.P., Davis B.C.;

"Genomic Organization of Mouse and Human 65 kDa FK506-binding prot
"Genomic Organization of the FKBP Multigene Family.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

E EMBL; AF456413; AAL57621.1; -.

R EMBL; AF456413; AAL57621.1; -.

R EMBL; AF456412; AAL57621.1; JOINED.

InterPro; IPR0002048; EF-hand.

R InterPro; IPR0001179; FKBP.

R InterPro; IPR0001179; FKBP.

R Fam; PF000354; FKBP; 4.

R SMART; SM00054; EFH; 1.

R SMART; SM00054; EFH; 1.

R PROSITE; PS00014; ER TARGET; UNKNOWN 1.

R PROSITE; PS00014; FKBP PPIASE 2; UNKNOWN 1.

R PROSITE; PS00059; FKBP PPIASE 2; UNKNOWN 1.

R PROSITE; PS00059; FKBP PPIASE 3; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mu
                                                                                                                                       --- EINKVTF--FCCPFVSWRRWYPEGRGQ-LPQDSNDSPPADL 342
                                                                                                                                                                             485 ENLFEIMDLDKNGEVPEEFFSDFLKAQVS-----EGKGRFLPGVDREKSIADM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.5%; Score 1022; DB 11; Length 55.8%; Pred. No. 1.2e-78; ive 58; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, I
01-JUN-2002 (TrEMBLrel. 21, I
65 kDa FK506-binding protein.
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Best Local Similarity 55.8<sup>†</sup>
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Wouse)
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                                                                                                                                       300 PNLFE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                  NPKDSISIENKVVPENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVWHKPDSCNTTSKKGDFIKYHYNCSMLDGTLLFSSHEYETPQQVTLGSSKVIEGLDTGL 425
                                                                                                                                                                                                         237
                                                                                                                                                                                                                                           260 NPKDGITIENQLVPESCERRTQTGDFIRYHYNGTLLDGTLFDSSYSRNRTYDTYVGKGYV 319
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                                                                                                        320 IAGMDEGLLGVCTGERRRIIIPPHLGYGEEGRGKIPGSAVLVFDIHVADFHNPSDSVSIT
                                                                 I PGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGNI PGSAVLVFDIHVIDFHNPSDSISIT
                                                                                                                                                                                                  181 SHYKPPDCSVLSKKGDYLKYHYNASLL -- - DGTLLDSTWNLGKTYNIVLGSGQVVLGMDM
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Kenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 564;
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58.5%; Pred. No. 1e-82;
iive 48; Mismatches 80; Indels
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Last annotation update)
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R Interpro; IPR000248; ER target.
Interpro; IPR001179; FKBP PPIASE.
Pfam; PR00254; FKBP; 4.
SMART; SM00054; FKBP; 4.
SMART; SM00054; EKBP; 2.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS000454; FKBP PPIASE 2; UNKNOWN 2.
PROSITE; PS00454; FKBP PPIASE 2; UNKNOWN 2.
PROSITE; PS00454; FKBP PPIASE 3; 4.
SRQUENCE 564 AA; 62643 MW; 15312365HFFA771
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MEDLINE=20302564; PubMed=10842073;
Spokony R., Saint-Jeannet J.-P.;
"Xenopus FK 506-binding protein, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         early development.";
Mech. Dev. 94:205-208(2000).
EMBL; AF233672; AAF35906.1; -.
HSSP; P20081; 1YAT.
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSPNLFEEINK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 VSPNLFEEIDQ 507
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Q918P8;
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Q918P8
ID Q9181
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SEQUENCE FROM N.A.
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REMBL, AKOS1564; BAB15220.1; -. REMBL/GenBank/DDBJ databases.

RHSSP, Q00688; 1PBK.

InterPro; IPR001048; EF-hand.

RITERPRO; IPR001179; FKBP. 4.

RITERPRO; IPR001179; FKBP. 4.

REMBL; SMO014; EFH, Z.

ROSITE; PS00014; EFH, Z.

ROSITE; PS00014; ER TARGET; UNKNOWN 1.

RROSITE; PS00014; FKBP PPIASE.

RROSITE; PS00014; FKBP PPIASE.

RROSITE; PS00015; FKBP PPIASE.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
65kDa FKS06-binding protein.
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                                                                                                                                                                                                    Homo sapiens (Human)
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Mitchimori C., Morikawa N., Isogai T., Ota T., Yuri K., Nishikawa T.,
Masuho Y., Nagahari K.;
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Masuho Y., Nagahari K.;
Masuho Y., Nagahari K.;
Masuho Y., Nagahari K.;
Masuho Y., Nagahari K.;
Masuho Y., Nagahari Y.;
Masuho Y., Nagahari Y.;
Masuho Y., Nagahari Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y., Nishi Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TYGEIGWLIPGMDKGLLGMCVGEKRIITIPPFLAYGEDGDGKDIPGQASLVFDVALLDLH
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTN-2002 (TrEMBLrel. 2), Last annotation update)
Hypothetical 64.2 Kba protein (65 kba FK506-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IRR002048; EF-hand.
InterPro; IRR000866; ER target.
InterPro; IPR001179; FKEP_PPIase.
Pfam; PP00254; FKEP; 4.
SMART; SM00054; EFH; 2.
PROSITE; PS00014; EF, HAND; UNKNOWN 1.
PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
PROSITE; PS00014; FKEP_PPIASE 2; 4.
SROUTE; PS00059; FKEP_PPIASE 3; 4.
SEQUENCE 582 AA; 64305 WW; 04B25129A1D44D92 CRC64;
SEQUENCE FROM N.A.
Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Sait
Yamamoto J., Sugano S., Isogai T.;
"HRI human cDNA sequencing project.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Ottenweelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

HSR1, Ali3116, CAB61418-1; -.

HSR1, AD0688; LPBR.

InterPro; IPR002048; EF-hand.

InterPro; IPR001086; ER target.

InterPro; IPR001179; FKBP PPIase.

Pfam; PF00254; FKBP; 2.

Pfam; PF00254; FKBP; 2.

Pfam; PF00154; FKBP; 2.

PROSITE; PS00018; EF HAND; UNKNOWN 1.

PROSITE; PS00014; ER TARGET; UNKNOWN 1.

PROSITE; PS00014; ER TARGET; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 RG-VPGSAVILPEVELVSREDGLPTGYLFVWHKDPPANLFEDMDLNKDGEVPPEEFSTFI 299
                                                                                                                                                                                                                                                                                                 87 LRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQGYVIPGMDEGLLGVCIGEKRRIVVPPHLG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 DGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEVSPNLFE--EINK-----VTFF 312
                                                                                                                                                                                                                                                                                                                                                                                                                     61 YGENGTDSIGFLQGSAPLRPFRSGEGQPSLGREGGYGKTEPAYPQDPAVLGASVSSPVKW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IPGSAVLVFDIHVIDFHNPSDSISITSHYKPPD-CSVLSKKGDYLKYHYN 203
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                           51; Indels
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            InterPro; IPR000886; ER target.
InterPro; IPR001179; FKBP_PPIase.
Pfam; PP000246; efhand; 2.
Pfam; PF00024; FKBP; 2.
SMART; SM00054; EFP; 2.
PROSITE; PS00014; ER TAND; UNKNOWN 1.
PROSITE; PS00014; ER TANGET; UNKNOWN 1.
PROSITE; PS00099; FKBP PPIASE 3; 2.
SRQUENCE 355 AA; 38950 MW; DBECF4B8618BF54F CRC64;
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Last annotation update)
                                                                                                                                                                                                                32.7%; Score 688; DB 4;
ilarity 42.5%; Pred. No. 1.8e-50;
Conservative 50; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence
1-MAX-2002 (TrEMBLrel. 20, Last annotati
Hypothetical 28.9 kDa protein (Fragment).
DKF2EP58610821.
InterPro; IPR002048; EF-hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 CCPFVSWRRWYPEGRGOL 330
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                                                                                                                                                                                                                                                                                                                                                                                   147 YGEEGRGN------
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Hypothetical protein
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Matches 135; Conserv
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SEQUENCE
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Q9UF89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 RTLSRPSETCNETTKGGDFVRYHYNCSLLDGTQLFTSHDYGAPQEATLGANKVIEGLDJG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 LREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNGEV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 TYVGSGWLIKGNDQGLLGMCPGBRRKIIIPPFLAYGEKGYGTVIPPQASLVFHVLLIDVH 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 NPKDAVQLETLELPPGCVRRAGAGDFWRYHYNGSLMDGTLFDSSYSRNHTYNTYIGQGYI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 IPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 IPGMDQGLQGACMGERRRITIPPHLAYGENGTGDKIPGSAVLIFNVHVIDFHNPADVVEI 382
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 11, Last annotation update)
CDNA: FLJ22221 fis, clone HRC01651.
Homo saplens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
47.5%; Score 1000.5; DB 4; Length 582;
Best Local Similarity 55.1%; Pred. No. 8.1e-77;
Matches 189; Conservative 60; Mismatches 73; Indels 21;
                                                                                                                 Rulten S., Kinloch R.A., Robinson C., Gettins L., Kay J.E.;
"The Human FK506-Binding Protein Repertoire.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016467; AA441647.1; -.
REMEL; AF337909; AA41647.1; -.
RINEEPRO; IPR0012048; EF-hand.
RINEEPRO; IPR001309; EMBP Plase.
RinterPro; IPR001179; FKBP PPlase.
Pfam; PF00036; efhand; 2.
Rem; PF0054; FKBP; 4.
RP03ITE; PS00014; ER_TARGET; UNKNOWN 1.
RROSITE; PS00014; ER_TARGET; UNKNOWN 1.
RROSITE; PS00014; ER_TARGET; UNKNOWN 1.
RROSITE; PS00014; ERPP PPLASE 2; UNKNOWN 1.
RROSITE; PS00014; ERPP PPLASE 2; UNKNOWN 1.
RROSITE; PS00014; ERPP PPLASE 2; UNKNOWN 1.
RROSITE; PS00016; ERBP PPLASE 2; UNKNOWN 1.
RROSITE; PS00016; ERBP PPLASE 2; UNKNOWN 1.
RROSITE; PS00016; FKBP PRASE 2; UNKNOWN 1.
                                                                                                                        Gettins L., Kay J.E.;
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TISSUB=BRAIN;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                  SEQUENCE FROM N.A.
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                                                                                                       TISSUE=BRAIN;
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us-09-225-502-8.rspt

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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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SEQUENCE 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 MDEGLIGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSISITSH 182
                                                                                                                                                                         178 SITSHYKPPD-CSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLGSGQVVLGMD 236
                                                                                                                                                                                              121 TGLQGMCVGERRQLIVPPHLAHGESGARG-VPGSAVLLFEVELVSREDGLPTGYLFVWHK 179
                                                                                                                                                                                                                                                        237 MGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELVAGLPEGYMFIWNG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 YVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEGRGN-IPGSAVLVFDIHVIDFHNPSDSI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                               Gaps
                                                                                                              Amano T., Yoshizato K.; "Isolation of genes involved in intestinal remodeling during anuran metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FK506-binding protein (Fragment).
Sanopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
27.2%; Score 572.5; DB 4; Length 262; 48.9%; Pred. No. 8.4e-41; ive 45; Mismatches 49; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF170336, AAK11511.1; --
HSSP, 000688, IPBK.
InterPro, IPR01179, FKBP_PPIase.
PROSITE; PS00454; FKBP, 1.
PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 137 137 DC3E6ACABB24F625 CRC64;
                                                                                                                                                                                                                                                                                                                                          297 EVSPNLFE--EINK-----VTFFCCPFVSWRRWYPEGRGQL 330
                                                                                                                                                                                                                                                                                                                                                                   01-00N-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 AA.
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O16309,
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YKPPDC-SVLSKKGDYL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 WPPGVQTAKAVTGDYV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74; Conservative
                                             Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
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                        Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 EGLLGVCIGEKRRIVVPPHLGYGEEGRGNIPGSA-VLVFDIHVIDFHNP-----SDS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90; Indels 11; Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Sammons L., Wohldmann P.;
"The sequence of C. elegans cosmid COSC8.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 MGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016430; AAB65370.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1 protein.
261 AA; 29080 MW; 545A8B82B1BB26AD CRC64;
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01-MAY-1997 (TYEMBLrel. 03, Last sequence update)
01-DEC-2001 (TYEMBLrel. 19, Last annotation update)
Hypothetical 29.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%; Score 353.5; DB 32.6%; Pred. No. 4e-22; tive 52; Mismatches 9
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PROSITE, PS0014, FR TAKGET; UNKNOWN 1.
PROSITE; PS00454; FKBP PPIASE 2; UNKNOWN 1.
PROSITE; PS50059; FKBP PPIASE 3; 2.
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InterPro, IPR000886, ER target.
InterPro, IPR001179, FKBP_PPIase.
                                                                                                                                                                                                                                                                        MEDLINE=99069613; PubMed=9851916;
Hypothetical 29.1 kDa protein.
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les 74; Conservative
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Search completed: April 26, 2003, 06:55:47 Job time: 35.1369 seca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 YVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEG--RGNIPGSAVLVFDIHVIDFH----- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NPSDSISITSHYK-PPDCSVLSKKGDYLKYHYNASLLDGTLLDSTWNLGKTYNIVLG 227
                                                                                                                                                                                                                                                                                                                                                                                                          16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 KDEDGLEIKIIRPIKAEKCPIKSQDGDVLDQWYKLSDKDGKEIGSNFNK-KPYTFTLGKG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 SGOVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                 Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                          95; Indels
                                                                                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U80445; AAB37799.1; -.
HSSP; P20071; BL4.
InterPro; IPR00886; ER target.
InterPro; IPR001179; FKBP_PPIase.
                                                                                                                           Du Z., Le T.T.;
"The sequence of C. elegans cosmid CSOF2.";
Submitted (JAN-1997) to the EMBL/GenBgnk/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          29937 MW; 90B79FD4FF978A2D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAP-2002 (TremBLrel. 20, Last annotation update)
C50F2.6.
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
16.3%; Score 344; DB 5;
Best Local Similarity 33.9%; Pred. No. 2.6e-21;
Matches 80; Conservative 45; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 AA.
                                                                                                                                                                                                                                                                                         PREMI, PRO0244, FKBP, 2.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
PROSITE; PS000454; FKBP PPIASE 2; UNKNOWN 2.
PROSITE; PS00059; FKBP PPIASE 3; 2.
Hypothetical protein.
SEQUENCE 264 AA; 29937 MW; 90B79FD4FF97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
 SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                        Waterston R.;
"Direct Submission.";
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 KDSISIENKVV----PENCERISQSGDFLRYHYNGTLLDGTLFDSSYSRNRTFDTYIGQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KDEDGLEIKIIRPIKAEKCPIKSQDGDVLDQWYKLSDKDGKEIGSNFNK-KPYTFTLGKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 YVIPGMDEGLLGVCIGEKRRIVVPPHLGYGEEG--RGNIPGSAVLVFDIHVIDFH---- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 NNEVIKGMDIAMTGMCEGERRQVVIPSDFGYGDDGRAPAIPGKARLYFDITLEKLI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 SGQVVLGMDMGLREMCVGEKRTVIIPPHLGYGEAGVDGEVPGSAVLVFDIELLELV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
16.3%; Score 344; DB 5; Length 30
Best Local Similarity 33.9%; Pred. No. 3.1e-21;
Matches 80; Conservative 45; Mismatches 95; Indels
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Du Z., Le T.T.;
"The sequence of C. elegans cosmid C50F2.";
"The sequence of C. to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                 Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; U80445; AAK68259.1; -.

InterPro; IPR000886; ER target.

InterPro; IPR00194; FKBP-PPIASE.

PROSITE; PS00014; ER TARGET; UNKNOWN 1.

PROSITE; PS00054; FKBP-PPIASE 2; UNKNOWN 2.

PROSITE; PS50059; FKBP-PPIASE 3; 2.

Hypothetical protein.

SEQUENCE 300 AA; 34160 MW; A70252F2736CF36C CRC64;
                                                                                                                                                                                                                                                          Materston R.;
"Direct Submission."; '
                                                                                                                                                                  [3]
SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
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